

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 11:49:00 ; Search time 5161.56 Seconds
(without alignments)
13086.780 Million cell updates/sec

Title: US-10-735-098-7

Perfect score: 2262

Sequence: 1 atgtgtaaacgaattatgg.....tcgaggaggtggaataatga 2262

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103.8	4.6	908	28	AZ548467
c 2	101.8	4.5	434	14	CA745444
c 3	100.8	4.5	263	13	BU005139
4	100.4	4.4	395	29	CE760553

c 5	100.4	4.4	843	28	AZ551618
c 6	100.2	4.4	232	29	CG321416
c 7	100.2	4.4	233	12	BU454017
c 8	98.8	4.4	265	14	CA607797
c 9	98.8	4.4	880	28	AZ529191
10	98.6	4.4	264	13	BQ241566
11	98.6	4.4	332	14	CA566759
12	98.6	4.4	575	10	BF707975
13	98.4	4.4	960	28	CC143364
14	98.2	4.3	594	12	BM167059
15	98.2	4.3	612	28	BZ149404
c 16	98.2	4.3	739	28	BZ220379
c 17	98.2	4.3	799	28	BZ201507
c 18	98.2	4.3	1096	14	CK206118
c 19	97.6	4.3	605	28	BZ222147
c 20	97.6	4.3	665	13	BU432980
21	97.4	4.3	341	29	CE510654
22	97	4.3	278	13	BQ460618
c 23	97	4.3	617	14	CA743799
c 24	97	4.3	691	28	BH040136
c 25	97	4.3	890	28	BH146886
c 26	97	4.3	906	28	BH153606
c 27	96.6	4.3	531	14	CD913362
c 28	96.6	4.3	546	28	AZ600777
c 29	96.2	4.3	289	14	CA716220
c 30	96.2	4.3	340	13	BQ462203
c 31	96.2	4.3	471	12	BM166650
c 32	96.2	4.3	477	14	CD311846
c 33	96	4.2	622	13	BU418103
c 34	95.8	4.2	302	9	AA572217
c 35	95.4	4.2	311	14	CA699402
c 36	95.4	4.2	406	28	AZ509483
c 37	95.4	4.2	924	13	BQ925195
c 38	95.2	4.2	548	9	AI746770
c 39	95.2	4.2	675	28	BZ104011
c 40	95.2	4.2	3743	11	AK048184
c 41	94.4	4.2	537	14	CF380795
c 42	94.2	4.2	223	13	CA022136
c 43	94.2	4.2	866	28	AZ527885
c 44	94.2	4.2	877	28	AZ531291
c 45	94.2	4.2	912	28	AZ551092

ALIGNMENTS

RESULT 1
AZ548467
LOCUS
DEFINITION
ENTEX30TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.
ACCESSION
AZ548467
VERSION
AZ548467.1 GI:11172102
KEYWORDS
GSS.
SOURCE
Entamoeba histolytica
ORGANISM
Entamoeba histolytica
REFERENCE
1 (bases 1 to 908)
AUTHORS
Loftus B., Van Aken, S. and Fraser, C.
TITLE
Determination of clone end sequences from Entamoeba histolytica
JOURNAL
HM1:IMSS sheared DNA library
COMMENT
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
Seq primer: M13-Reverse
Class: shotgun

AZ548467
ENTEX30TR Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.
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SOURCE
Entamoeba histolytica
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Unpublished (2000)
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
Seq primer: M13-Reverse
Class: shotgun

AZ551618 ENTVD54TR
CG321416 GGYBI53TV
BU454017 BU454017
CA607797 wrl.pk008
AZ529191 ENTBV68TR
BQ241566 TAE05003E
CA566759 K0405E07-
BF707975 A634 LE A
CC143364 NDL.32A13
BM167059 EST569582
BZ149404 CH230-395
BZ220379 CH230-312
BZ201507 CH230-445
CK206118 FGAS01769
BZ222147 CH230-361
BU432980 603221001
CE510654 tigr-gss-
BQ460618 HA06H01F
CA743799 wrl18.pk0
BH040136 RPCT-24-2
BH146886 ENTPK48TF
BH153606 ENTPS83TF
CD913362 G550.1250
CA716220 wdk3c.pk0
BM166650 EST569173
CD311846 StrPn691.
BU418103 603959413
AA572217 v151e08.r
CA699402 wlk8.pk00
AZ509483 LM0352019
BQ925195 AGENCOURT
AI746770 ul07c01.y
BZ104011 CH230-227
AK048184 Mus muscu
CF380795 lac78f12.
CA022136 HZ42E07r
AZ527885 ENTPCA79TR
AZ531291 ENTPBQ34TR
AZ551092 ENTPFJ22TF

RESULT 3
BU0051139/c
LOCUS
DEFINITION QG7D20.Y9.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
BU0051139
ACCESSION QG7D20.Y9.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
VERSION BU0051139
KEYWORDS EST.
SOURCE BU0051139.1 GI:22439534
ORGANISM Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Lactuca.
REFERENCE 1 (bases 1 to 263)
AUTHORS Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
JOURNAL http://compgenomics.ucdavis.edu/
COMMENT Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@catc.org [michelmore@vegmail.ucdavis.edu]
singletton, see http://cgpdb.ucdavis.edu/ for details.
Plate: QGG7 row: D column: 20.

FEATURES
Location/Qualifiers
1..263
/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QG7D20"
/lab_host="E.coli"
/clone_lib="QG_EFGHJ lettuce serriola"
/note="Vector: pBRCDNA5FIAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_SEQ-Not found"

ORIGIN
Query Match 4.5%; Score 100.8; DB 13; Length 263;
Best Local Similarity 66.7%; Pred. No. 9.4e-10;
Matches 144; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 1391 AACCAAGCGCGAGATTAAGCGGAGGATGAAGGGTGCAGGGCTTGTATACGACGAAG 1450
Db 227 AAG 168
QY 1451 AAAGCGAAGACGAAGCGCTAGAACGAGCGCGCGAGAGAGCGAACTTCCGAGAGG 1510
Db 167 AAG 108
QY 1511 ATATGCGAGAGACGAAGCAACCGCCGAGAGAGAAACCGAGAGAGATTGATCAAGCG 1570
Db 107 AAG 48
QY 1571 AAGAGAGAGAGTTGAGAACCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1606
Db 47 AAG 12

RESULT 4
CE760553
LOCUS
DEFINITION tigr-gss-dog-17000369997532 Dog Library Canis familiaris genomic, genomic survey sequence.
CE760553
ACCESSION CE760553.1 GI:37101172
VERSION
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 395)
AUTHORS Kirkness, E.F., Bafna V., Halpern, A.L., Levy, S., Remington, K., Rusk, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.

TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1..395
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN
Query Match 4.4%; Score 100.4; DB 29; Length 395;
Best Local Similarity 63.0%; Pred. No. 1.2e-09;
Matches 155; Conservative 0; Mismatches 91; Indels 0; Gaps 0;
QY 1391 AACCAAGCGCGAGATTAAGCGGAGGATGAAGGGTGCAGGGCTTGTATACGACGAAG 1450
Db 83 AAG 142
QY 1451 AAAGCGAAGACGAAGCGCTAGAACGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 1510
Db 143 AAG 202
QY 1511 ATATGCGAGAGACGAAGCAACCGCCGAGAGAGAAACCGAGAGAGTTGATCAAGCGC 1570
Db 203 AAG 262
QY 1571 AAGAGAGAGAGTTGAAGACCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1630
Db 263 AAG 322
QY 1631 GCAGCA 1636
Db 323 GAGGAA 328

RESULT 5
AZ551618/c
LOCUS
DEFINITION ENT5V4T8 Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, genomic survey sequence.
ACCESSION AZ551618
VERSION AZ551618.1 GI:111176919
KEYWORDS GSS.

[illegible]

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Matches 147; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1391 AACCAAGCGGAGATTAAGGGGAGGATCAAGAGGGTGCAGCGTGTGATACGACGAAG 1450
Db 226 AAGAGAGAGAGAGAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 167

QY 1451 AAAGCGAGACGAGCGGTAGAGACGAGCGCGGCGGAAGAGAGAGAGAGAGAGAGAG 1510
Db 166 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 107

QY 1511 ATATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1570
Db 106 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 47

QY 1571 AAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1615
Db 46 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2

RESULT 7
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LOCUS
DEFINITION
  BJ454017 K. Sato unpublished cDNA library, cv. Akashinriki
  vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone
  baak45j15 5', mRNA sequence.
ACCESSION
  BJ454017
VERSION
  BJ454017.1 GI:21132592
KEYWORDS
  EST.
SOURCE
  Hordeum vulgare subsp. vulgare
  ORGANISM
    Hordeum vulgare subsp. vulgare
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Pooideae; Triticeae; Hordeum.
  1 (bases 1 to 233)
REFERENCE
  Sato, K., Saisho, D. and Takeda, K.
  Barley EST sequencing project in NIG and Okayama Univ
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
FEATURES
  Location/Qualifiers
    1..233
      /organism="Hordeum vulgare subsp. vulgare"
      /mol_type="mRNA"
      /cultivar="Akashinriki"
      /sub_species="vulgare"
      /db_xref="taxon:112509"
      /clone="baak45j15"
      /tissue_type="leaves"
      /dev_stage="vegetative stage"
      /clone_lib="K. Sato unpublished cDNA library, cv.
      Akashinriki vegetative stage leaves"
ORIGIN
  Query Match 4.4%; Score 100.2; DB 12; Length 233;
  Best Local Similarity 65.3%; Pred. No. 1.2e-09;
  Matches 147; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 1391 AACCAAGCGGAGATTAAGGGGAGGATGAGAGGGTGCAGCGTGTGATACGACGAAG 1450
Db 228 AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 169

QY 1451 AAAGCGAGACGAGCGGTAGAGACGAGCGCGGCGGAAGAGAGAGAGAGAGAGAGAG 1510
Db 168 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 109

QY 1511 ATATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1570
Db 108 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 49

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QY 1571 AAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1615
Db 48 AAGATGAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4

RESULT 8
CA607797/c
LOCUS
DEFINITION
  CA607797 wrl.pk0082.f4 wrl Triticum aestivum cDNA clone wrl.pk0082.f4 5',
  end. mRNA sequence.
ACCESSION
  CA607797
VERSION
  CA607797.1 GI:25162959
KEYWORDS
  EST.
SOURCE
  Triticum aestivum (bread wheat)
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Pooideae; Triticeae; Triticum.
  1 (bases 1 to 265)
REFERENCE
  Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
  Miao, G., Caraher, N. and Hanafey, M.K.
  DuPont Wheat cDNA Sequence
  Unpublished (2002)
  Contact: Scott V. Tingey
  Crop Genetics
  E. I. DuPont de Nemours and Company
  1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
  Tel: 302-631-2602
  Fax: 302-631-2607
  Email: Scott.V.Tingey@USA.dupont.com
  Seq primer: M13.
FEATURES
  Location/Qualifiers
    1..265
      /organism="Triticum aestivum"
      /mol_type="mRNA"
      /db_xref="taxon:4565"
      /clone="wrl.pk0082.f4"
      /tissue_type="root"
      /clone_lib="wrl"
      /note="Vector: pbluescript SK+; Site.1: EcoRI; Site.2:
      XhoI; Wheat (Triticum aestivum L.) root; 7 day old
      seedling, light grown"
ORIGIN
  Query Match 4.4%; Score 98.8; DB 14; Length 265;
  Best Local Similarity 62.6%; Pred. No. 2.4e-09;
  Matches 142; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 1389 TAACCAAGCGGAGAGATTAAGGGGAGGATGAAGAGGGTGCAGCGTGTGATACGACGA 1448
Db 230 TGAAGNTGACGANGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATA 171

QY 1449 AGAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1508
Db 170 AGAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 111

QY 1509 GGAATATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1568
Db 110 AGANGATGANGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 51

QY 1569 CGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1615
Db 50 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4

RESULT 9
AZ529191/c
LOCUS
DEFINITION
  ENTBV68TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
  genomic, genomic survey sequence.
ACCESSION
  AZ529191
VERSION
  AZ529191.1 GI:11081835

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KEYWORDS	GSS.
SOURCE	Entamoeba histolytica
ORGANISM	Entamoeba histolytica
REFERENCE	Eukaryota; Entamoebidae; Entamoeba.
AUTHORS	Loftus, B., Van Aken, S. and Fraser, C.
TITLE	Determination of clone end sequences from Entamoeba histolytica
JOURNAL	HMI:IMSS sheared DNA library
COMMENT	Unpublished (2000) Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 3543 Email: b.loftus@tigr.org Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library Seq primer: M13-Reverse Class: shotgun High quality sequence start: 17 High quality sequence stop: 673.
FEATURES	Location/Qualifiers
Source	1. .880 /organism="Entamoeba histolytica" /mol_type="genomic DNA" /strain="HMI:IMSS" /db_xref="taxon:5759" /clone_lib="Entamoeba histolytica Sheared DNA" /note="Vector: pHS1; Site 1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaubin and B. Barrel, Oxford University Press, 1999)."
ORIGIN	Query Match 4.4%; Score 98.8; DB 28; Length 880; Best Local Similarity 64.3%; Pred. No. 2.9e-09; Matches 148; Conservative 0; Mismatches 82; Indels 0; Gaps 0; QY 1386 AAGTAAACCAAGCGGAGATAAAGCGGAGATGAAGGGTGCAGGGCTTGATAACGA 1445 Db ATATATATTAGACCGGAGAGAGACGACGAGAGATGAAGCGACGAGAGACGA 707 QY 1446 CGAAGAAACGAGACGAGCCGTAGACGAGCGGCGGAGAGAGACGAACTTCGA 1505 Db AGATGAAGAGACGAGACGAGCAGATGACGAGAGAGACGAGAGAGACGAGAGAG 647 QY 1506 AGAGGATATGGGAGACGAGACGACCAACCGCGGAGAGAGAACCGAGAGCTTGATGA 1565 Db AGACGAG 587 QY 1566 AGCCGAG 1615 Db AGACGAGAGAGATGAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537
RESULT 10	
LOCUS	BQ241566 264 bp mRNA linear EST 03-MAY-2002
DEFINITION	TAE05003E07R Tae05 Triticum aestivum cDNA clone TaE05003E07R, mRNA sequence.
ACCESSION	BQ241566
VERSION	BQ241566.1 GI:20437442
KEYWORDS	EST.

SOURCE	Triticum aestivum (bread wheat)
ORGANISM	Triticum aestivum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
AUTHORS	1 (bases 1 to 264)
TITLE	Wheat functional genomics - Glenlea developing seeds cDNA libraries
JOURNAL	Cloutier, S.
COMMENT	Unpublished (2002) Contact: Dr. Sylvie Cloutier Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9 Tel: (204) 983-2340 Fax: (204) 983-4604 Email: scloutier@agr.gc.ca was cloned directionally, not all sequences generated with reverse primer were from the 5' end (same with forward primer and 3' end). Average insert size is >2.0 Kb Plate: 003 row: E column: 07 Seq primer: M13 Reverse.
FEATURES	Location/Qualifiers
Source	1. .264 /organism="Triticum aestivum" /mol_type="mRNA" /cultivar="Glenlea" /db_xref="taxon:4565" /clone="TAE05003E07R" /tissue_type="developing seeds" /dev_stage="5 days after anthesis" /lab_host="E. coli DH10B" /clone_lib="TAE05" /note="Vector: pSPORT-P (Invitrogen Technologies); Site 1: NotI; Site 2: MluI; mRNA obtained from wheat seeds of cultivar Glenlea 5 days post-anthesis"
ORIGIN	Query Match 4.4%; Score 98.6; DB 13; Length 264; Best Local Similarity 64.9%; Pred. No. 2.6e-09; Matches 146; Conservative 0; Mismatches 79; Indels 0; Gaps 0; QY 1391 AACCAAGCGCAAGTAAGGGAGGATGAAGGGTGACGGCTTGATACGACGAAG 1450 Db AAAGAAGAAGTGGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 81 QY 1451 AAAGCGACGACGAGCCGTAGAGACGAGAGCGGCGGAGAGCAAACTTCGAAGAG 1510 Db AGAAAAAG 141 QY 1511 ATATGGCGGAGACGAGAGAGCAACCGCGGAGAGAGAAACCGAGAGTTGATGACCG 1570 Db AAGAAGAAG 201 QY 1571 AAGAGGAGAGAGTTGAAGACCCGAGAGAAAATCGCCGCGAGAG 1615 Db AAGAAGAAG 246
RESULT 11	
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DEFINITION	K0405E07-SN NTA Mouse Mesenchymal Stem Cell cDNA Library (Long) Mus musculus cDNA clone NIA:K0405E07 IMAGE:30059574 5', mRNA sequence.
ACCESSION	CA566759
VERSION	CA566759.1 GI:25111430
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 332)
TITLE	Piao, Y., Kargul, G. J., Dudekula, D. B., Qian, Y., Luo, A., Carter, M. G., Umezawa, A. and Ko, M. S. H.
TITLE	Systematic Analyses of NTA Mouse Mesenchymal Stem Cell cDNA Library

JOURNAL
COMMENT

(Long)

Unpublished (2001)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0405 row: E column: 07
Seq primer: M13 Reverse
High quality sequence stop: 332
POLYA-No.

FEATURES
source

Location/Qualifiers
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/tissue_type="Mesenchymal stem cell"
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/lab_host="DH10B"
/clone_lib="NIA Mouse Mesenchymal Stem Cell cDNA Library (Long)"
/note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cdna). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Akihiro Umezawa (Keio University School of Medicine, Japan). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGGCGGCGCCCTTTTCTTTT-3'] from 2.2 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker IL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."

ORIGIN

Query Match 4.4%; Score 98.6; DB 14; Length 332;
Best Local Similarity 64.9%; Pred. No. 2.7e-09;
Matches 146; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1391 AACCAAGCGGAGATTAAGGGGAGGATGAAGAGGGTGCAGGGCTTGATTAACGACGAAG 1450
3 AAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 62

QY 1451 AAAGCGAAGCGAGCGGTAGAACGACGAGCGCGGAGAGAGAGAACTTCCGAGAGG 1510
63 AAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 122

QY 1511 ATATGGCGAAGACGAAGAACCCCGGAGAGAGAAACCGGAGAGAGTTGATGAAGCGG 1570
123 AAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 182

QY 1571 AAGAGGAGGAGTTGAGAAACCCGAGAGAAAATCCCGGAGAG 1615
183 AAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 227

RESULT 12

BF707975
LOCUS 575 bp mRNA linear EST 12-JUN-2002

DEFINITION

AC34 LE Aplysia metacerebral cell cDNA library Aplysia californica cDNA 5', mRNA sequence.

ACCESSION

BF707975

VERSION

BF707975.1 GI:18002301

KEYWORDS

EST.

SOURCE

Aplysia californica (California sea hare)

ORGANISM

Aplysia californica

REFERENCE

1 (bases 1 to 575)

AUTHORS

Sadreyev,R.I., Meleshkevich,E.A., Matz,M.V., Panchin,Y.V. and Moroz,L.L.

TITLE

Characterization of the gene pool expressed in the individual identified neuron

JOURNAL

Unpublished (2001)

COMMENT

Contact: Sadreyev RI
The Whitney Laboratory
University of Florida
9505 Ocean Shore Blvd., St Augustine, FL 32080, USA
Tel: 904 461 4044
Fax: 904 461 4008
Email: sadreyev@whitney.ufl.edu

FEATURES

Location/Qualifiers
1. .575
/organism="Aplysia californica"
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ORIGIN

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Best Local Similarity 64.9%; Pred. No. 3e-09;
Matches 146; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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Db

105 AAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 164

QY

1451 AAAGCGAAGCGAGCGGTAGAACGACGAGCGCGGAGAGAGAGAACTTCCGAGAGG 1510

Db

165 AAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 224

QY

1511 ATATGGCGAAGACGAAGAACCCCGGAGAGAGAAACCGGAGAGTTGATGAAGCGG 1570

Db

225 AAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 284

QY

1571 AAGAGGAGGAGTTGAGAAACCCGAGAGAAAATCCCGGAGAG 1615

Db

285 AAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAGAGAAG 329

RESULT 13

CC143364 960 bp DNA linear GSS 16-APR-2003

LOCUS

NDL.32A13.T7 Notre Dame Liverpool Aedes aegypti genomic clone

DEFINITION

NDL.32A13, genomic survey sequence.

ACCESSION

CC143364

VERSION

CC143364.1 GI:30012419

KEYWORDS

GSS.

SOURCE

Aedes aegypti (yellow fever mosquito)

ORGANISM

Aedes aegypti

REFERENCE

1 (bases 1 to 960)

AUTHORS

Nukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.

TITLE

Loftus,B., Shetty,J., Knudson,D. and Severson,D.

JOURNAL

BAC end sequencing of Aedes aegypti Unpublished (2003)

JOURNAL
COMMENT

Unpublished (1999)
 Other GSSs: CH230-395M1.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the rat BAC library CHORI-230
 (<http://www.chori.org/bacpac/rat230.htm>). For BAC library
 availability, please contact Pieter de Jong (pdjong@mail.cho.org).
 Clones may be purchased from BACPAC Resources
 (<http://www.chori.org/bacpac/oreringinformation.htm>). BAC end
 page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
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 Seq primer: SP6
 Class: BAC ends.
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 CHORI-230 Rat (BN/SSHsd/MCW) BAC library produced by
 Pieter de Jong"

FEATURES

source

ORIGIN

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Query Match      4.3%;  Score 98.2;  DB 28;  Length 612;
Best Local Similarity 64.1%;  Pred. No. 3.6e-09;
Matches 148;  Conservative 0;  Mismatches 83;  Indels 0;  Gaps 0;

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Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1455 CGACGACGAGCCGTAGAGCGAAGCGGCGGCGGAGAGACGAACTTCGAGAGAGGATAA 1514
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1515 TGGCGAGACGAGAGAGCAACCGCCGAGAGAGAAACCGAGAGTTGATGAGCCGAGA 1574
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 277  GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 336
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1575 GGAGGAGTTGAAGAACCGGAGAAATCGCCGACAGAGGCAACGCGG 1625
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QY 337  AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 387
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Search completed: August 25, 2004, 05:21:12
 Job time : 5163.56 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:53:30 ; Search time 7964.58 Seconds
(without alignments)
11558.757 Million cell updates/sec

Title: US-10-735-098-9
Perfect score: 2124
Sequence: 1 atgtgtaacacgaattatgg.....acaaggaggcaacacgatga 2124

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_or.*
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- 22: em_ov.*
- 23: em_pat.*
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- 25: em_pl.*
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- 28: em_un.*
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- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
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- 36: em_htg_mam.*
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- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2124	100.0	2124	1	AF123383
2	2124	100.0	2124	6	A98976
3	2124	100.0	2124	6	BD074759
4	1562.4	73.6	2169	1	AF123382
5	1562.4	73.6	2169	6	A98970
6	1562.4	73.6	2169	6	BD074756
7	1516.8	71.4	326301	1	NMA6Z2491
8	1499.8	70.6	2226	1	AF123380
9	1499.8	70.6	2226	6	A98972
10	1499.8	70.6	2226	6	BD074757
11	1416	66.7	2519	1	AF072890
12	1375.4	64.8	9955	1	AE002504
13	1375.4	64.8	349980	6	AX044033
14	1296.2	61.0	2277	1	AF022781
15	1296.2	61.0	2277	6	A98968
16	1296.2	61.0	2277	6	BD074755
17	1296.2	61.0	5691	1	AF049349
18	1293	60.9	2537	1	AF031432
19	1291.8	60.8	2262	1	AF123381
20	1291.8	60.8	2262	6	A98974
21	1291.8	60.8	2262	6	BD074758
22	497.6	23.4	1000	6	AX081510
23	497.6	23.4	1000	6	AX374691
24	231.8	10.9	3398	1	NMLBPAG
25	105.8	5.0	13297	10	AF317727
26	105.8	5.0	179685	10	AC122056
27	104.8	4.9	266939	2	AC098663
28	104.6	4.9	3300	6	AX685922
29	104.6	4.9	3300	6	AX685922
30	104.6	4.9	224784	2	AC110522
31	103.6	4.9	196963	2	AC133659
32	103.4	4.9	173949	10	AC132100
33	103.4	4.9	187930	2	AC124191
34	103.2	4.9	194060	2	AC125897
35	103	4.8	163710	2	AC112834
36	103	4.8	177128	2	AC113041
37	103	4.8	222469	10	AC140386
38	103	4.8	224843	2	AC147135
39	103	4.8	240033	2	AC133684
40	103	4.8	251725	2	AC094726
41	102.8	4.8	171477	2	AC102467
42	102.6	4.8	173556	2	AC074388
43	102.4	4.8	123180	10	AL672005
44	102.4	4.8	232224	2	AC110149
45	102.4	4.8	251960	2	AC107279

ALIGNMENTS

RESULT 1	AF123383	Neisseria meningitidis strain 881607	DNA	linear	BCT 24-MAY-1999
LOCUS	AF123383	precursor (lbpB) gene, complete cds.			
DEFINITION	AF123383				
ACCESSION	AF123383.1	GI:4884692			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					

Sequence variability of the meningococcal lactoferrin-binding protein lbpB

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Gene 231 (1-2), 105-110 (1999)
99250255
10231574
2 (bases 1 to 2124)
Petersson, A., van der Biesen, J., Joosten, V., Hendriksen, J. and Tomassen, J.
Direct Submission
Submitted (26-JAN-1999) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
Location/Qualifiers

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source

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ORIGIN

Query Match 100.0%; Score 2124; DB 1; Length 2124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTAACCGAATTATGCGGCATGTCTTGTGCGCTTACTTTGGCATCTTGCAIC 60
DB 1 ATGTGTAACCGAATTATGCGGCATGTCTTGTGCGCTTACTTTGGCATCTTGCAIC 60

QY 61 GCGGCAATTCGCGTGCAGCTGTGTGCAATCAACGCGACCGGTACCCCGTCACT 120
DB 61 GCGGCAATTCGCGTGCAGCTGTGTGCAATCAACGCGACCGGTACCCCGTCACT 120

QY 121 TTCAAGTCTAAGGACGTTCCTCACTTCGCTCTCTCGCGGTCTTCGGTAGAAACACGCGG 180
DB 121 TTCAAGTCTAAGGACGTTCCTCACTTCGCTCTCTCGCGGTCTTCGGTAGAAACACGCGG 180

QY 181 GTCAACCGACCCCGCTTGGTGGGCAATGCGGCTGTGTGAGACGGAATATGCAACTTCT 240
DB 181 GTCAACCGACCCCGCTTGGTGGGCAATGCGGCTGTGTGAGACGGAATATGCAACTTCT 240

QY 241 GATAAGATGGCAATGATTTTCCAAATAGCAACAGCAAGAAAGCTGTGTTTAA 300
DB 241 GATAAGATGGCAATGATTTTCCAAATAGCAACAGCAAGAAAGCTGTGTTTAA 300

QY 301 GAGGAAGATATCTCTGTTTATACGTTTCAAAAAGATCAACGTCAGCAGCTTAAAGAT 360
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QY 361 AAAATTCGTCAACCAATCTTACGGCAAGCATTTACCACTCGGAAAGAAATAAAAA 420
DB 361 AAAATTCGTCAACCAATCTTACGGCAAGCATTTACCACTCGGAAAGAAATAAAAA 420

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QY 481 GAGTGGACTTCAAAATTACAAGAGCTTACCAACCGGTTTGGTTATGACGGTTTGTATAT 540
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QY 541 TATTCCGAGAACATCTTTCGCAATCTTACCGAGCGGGAACGGTGAATATATTCGGCG 600
DB 541 TATTCCGAGAACATCTTTCGCAATCTTACCGAGCGGGAACGGTGAATATATTCGGCG 600

QY 601 AACTGGCAATATATGACCGATGCCATACGTATGCAACAGGAAAGAGGAGATCCTAGC 660
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QY 841 CCACTGACATTTACGACATTTACTGCAAAATTTGGACGGCAACCGCTTTACCGCGAGTGC 900
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QY 901 AAGTTTAAACACAGAGCTGAAGACCAATCAGCTGATTAAGAAATATTTGTTTTCATACC 960
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QY 961 GATGCCGATCAGCGGCTTGGAGCGGCTTTTTCGGCGATTAAGGGGAGAGCTTGC CGA 1020
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QY 1021 CGGTTTATCAGCAACGACAGACGCTTATTCGGCGTGTTCGCGGCAACCAAAAACAGAG 1080
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QY 1081 ACAGCAACCGCATCAGATACAAATCTGCGCTCTGCGCTCTGGAACCAACACCAAAATCTTG 1140
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Qy 1681 GAAGCGGACATTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 GAAGCGGACATTCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
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Qy 1981 AACTTCAAGCGGACAACTCTTCTGTAACAGCGGCTTTTATGCGCGCGAGAGAGAGAG 2040
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RESULT 2
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LOCUS A98976 2124 bp DNA linear PAT 26-JAN-2000
DEFINITION Sequence 9 from Patent WO9909176.
ACCESSION A98976
VERSION A98976.1 GI:6781936
KEYWORDS
SOURCE
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria
1 (bases 1 to 2124)
Petersson-Bernholm A. M. and Tomassen, J. P.
NEISSERIA LACTOFERRIN BINDING PROTEIN
Patent: WO 9909176-A 9 25-FEB-1999;
UNIV UTRECHT (NL); PETERSSON FERNHOLM ANNIKA (NL)
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4

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DEFINITION
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ACCESSION
AF123382
VERSION
AF123382.1 GI:4884690
KEYWORDS
Neisseria meningitidis
SOURCE
Neisseria meningitidis
ORGANISM
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
REFERENCE
1 (bases 1 to 2169)

AF123382 2169 bp DNA linear BCT 24-MAY-1999
Neisseria meningitidis strain m981 lactoferrin-binding protein precursor (lbpB) gene, complete cds.

AUTHORS Pettersson,A., van der Biesen,J., Joosten,V., Hendriksen,J. and Tommaassen,J.
TITLE Sequence variability of the meningococcal lactoferrin-binding protein lbpB
JOURNAL Gene 231 (1-2), 105-110 (1999)
MEDLINE 99250255
PUBMED 10231574
REFERENCE
AUTHORS Pettersson,A., van der Biesen,J., Joosten,V., Hendriksen,J. and Tommaassen,J.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-1999) Department of Molecular Cell Biology, Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
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RESULT 5
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DEFINITION Sequence 3 from Patent WO9909176.
ACCESSION A98970
VERSION A98970.1
KEYWORDS GI:6781930
SOURCE Neisseria meningitidis
ORGANISM Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 2169)
Petterson-Fernholm, A.M. and Tomassen, J.P.
TITLE NEISSERIA LACTOPEROXIN BINDING PROTEIN
JOURNAL Patent: WO 9909176-A 3 25-FEB-1999;
UNIV UTRECHT (NL); PETTERSSON FERNHOLM ANNKA MAR (NL)
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ORIGIN

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Query Match      73.6%; Score 1562.4; DB 6; Length 2169;
Best Local Similarity 84.5%; Pred. No. 0;
Matches 1835; Conservative 0; Mismatches 286; Indels 51; Gaps 5;

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QY	781	ACTCTGATGCGACGCTGATTAAATAACAGTATGTGCAAAAAGAGAGATGATCCTTAAAAA	840
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QY	901	AAAGTTAAACAGAGGTGAAGCAATCAAGCTGATTAAGATAATTTGTTTTCCATACC	960
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RESULT 6

BD074756

LOCUS

DEFINITION

Neisseria lactoferrin-binding protein.

ACCESSION

BD074756

VERSION

JP 2001514894-A/2.

KEYWORDS

unidentified

SOURCE

unclassified.

ORGANISM

1 (bases 1 to 2169)

REFERENCE

Felholm, A.M.P. and Thomasen, J.P.M.

Neisseria lactoferrin-binding protein

Patent: JP 2001514894-A 2 18-SEP-2001.

UNIVERSITY OF UTRICHT, TECHNOLOGY FOUNDATION

OS

Unidentified

PN

JP 2001514894-A/2

PD

18-SEP-2001

PF

10-AUG-1998

PR

15-AUG-1997

ANICA MARGARETA PETRUSON FELHOLM JOHANES PETRUS MARIA PI THOMASEN

PC

C12N15/09,A61K39/095,A61K39/395,A61K48/00,A61P31/12,C07K14/22,C07K16/12.

PC

C12N1/21,C12P21/02,C12P21/08,G01N33/15,G01N33/50,G01N33/68,PC

C12N15/00

CC

Strandedness: Double;

CC

Topology: Linear;

CC

Neisseria lactoferrin-binding protein

FT

Key

Location/Qualifiers

FT

source

1..2169

Location/Qualifiers

1..2169

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FEATURES

source

1..2169

Location/Qualifiers

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ORIGIN

Query Match

Best Local Similarity

Matches 1835;

Conservative

0;

Mismatches

286;

Indels

51;

Gaps

5;

QY

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QY 1933 CCGGAG 1992
Db 1978 CGTGAAG 2037
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RESULT 7
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LOCUS            Neisseria meningitidis serogroup A strain Z2491 complete genome;
DEFINITION      segment 6/7.
ACCESSION      NMA6Z2491
VERSION      AL162757.2
KEYWORDS      AL162757.2 GI:7380371
SOURCE      .
ORGANISM      Neisseria meningitidis Z2491
               Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
               Neisseriaceae; Neisseria.
REFERENCE      1 (bases 1 to 326301)
AUTHORS      Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,
               Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,
               Davies,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N.,
               Holroyd,S., Jagsels,K., Leather,S., Moule,S., Mungall,K.,
               Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,
               Skelton,J., Whitehead,S., Spratt,B.G. and Barrall,B.G.
               Complete DNA sequence of a serogroup A strain of Neisseria
               meningitidis Z2491
               Nature 404 (6777), 502-506 (2000)
JOURNAL      Nature 404 (6777), 502-506 (2000)
MEDLINE      20222556
PUBMED      10761919
REFERENCE      2 (bases 1 to 326301)
AUTHORS      Parkhill,J.
TITLE      Direct Submission
JOURNAL      Submitted (30-MAR-2000) Submitted on behalf of the Neisseria
               sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
               Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
COMMENT      Notes:
               Details of N. meningitidis sequencing at the Sanger Centre are
               available on the World Wide Web.
               (URL, http://www.sanger.ac.uk/Projects/N\_meningitidis/).
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AF123380
VERSION
AF123380.1
GI:4884686
KEYWORDS
Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.

REFERENCE
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FEATURES
source

1 (bases 1 to 2226)
Tomassen, A., van der Biezen, J., Joosten, V., Hendriksen, J. and
Tomassen, J.
Sequence variability of the meningococcal lactoferrin-binding
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Gene 231 (1-2), 105-110 (1999)
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2 (bases 1 to 2226)
Tomassen, A., van der Biezen, J., Joosten, V., Hendriksen, J. and
Tomassen, J.
Direct submission
Submitted (26-JAN-1999) Department of Molecular Cell Biology,
Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands
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ORIGIN

Query Match 70.6%; Score 1499.8; DB 1; Length 2226;
Best Local Similarity 83.3%; Pred. No. 7.6e-304;
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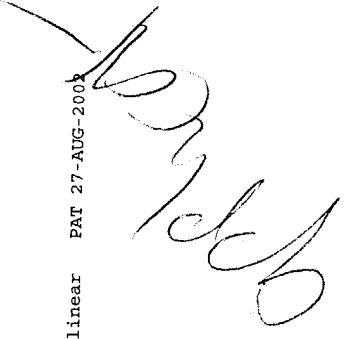
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unclassified.
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FEATURES
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Query Match
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Matches 1779; Conservative 0; Mismatches 317; Indels 39; Gaps 5;
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SOURCE ORGANISM Neisseria gonorrhoeae
Neisseria gonorrhoeae
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
REFERENCE 1 (bases 1 to 2519)
AUTHORS Biswas, G.D., Anderson, J.E., Chen, C.J., Cornelissen, C.N. and Sparling, P.F.
TITLE Identification and functional characterization of the Neisseria gonorrhoeae lbpB gene product
JOURNAL Infect. Immun. 67 (1), 455-459 (1999)
MEDLINE 95081783
PubMed 9864256
REFERENCE 2 (bases 1 to 2519)
AUTHORS Biswas, G.D., Anderson, J.E., Cornelissen, C.N. and Sparling, P.F.
TITLE Direct Submission
JOURNAL Submitted (18-JUN-1998) Medicine/ID, Univ. of N. Carolina, 521
Womack/CB 7030, Chapel Hill, N.C. 27599, USA
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DEFINITION Neisseria gonorrhoeae lactoferrin binding protein B precursor
(lbpB) gene, complete cds.
ACCESSION AF072890
VERSION AF072890.1 GI:4106392
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AE002504
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Thu Aug 26 10:18:19 2004

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VERSION
KEYWORDS
SOURCE
ORGANISM

AE002504 AE002098
AE002504.1 GI:7226785

Neisseria meningitidis MC58
Neisseria meningitidis MC58
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

REFERENCE
AUTHORS

1 (bases 1 to 9955)
Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,
Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,
Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,
Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,
Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,
Qin, H., Vamathevan, J., Gill, J., Scarlato, V., Massignani, V.,
Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
Rappuoli, R. and Venter, J.C.
Complete genome sequence of *Neisseria meningitidis* serogroup B
strain MC58
Science 287 (5459), 1809-1815 (2000)

JOURNAL
MEDLINE
PubMed
REFERENCE
AUTHORS

1 (bases 1 to 9955)
Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,
Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,
Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,
Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E.,
Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,
Qin, H., Vamathevan, J., Gill, J., Scarlato, V., Massignani, V.,
Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
Rappuoli, R. and Venter, J.C.
Direct Submission
Submitted (17-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
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QY      121  TTCAGTCTAAGGACGTTCCACTTTCGCTCCTGCGGGTCTTCGGTAGAACCAACGCGC 180
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QY      181  GTCAACCGACCCGCGTGTGGTGGCAATCGGGCTGTGAGACGGAATATTCGAATCTCT 240
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QY      241  GATAAGGATGGCAATGATTTTCCAAATAGCAACAGCAGAGAAAGAGCTCTCTTTAAA 300
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QY	1843	ATGCTGACAGAAATAATGATACACCCCGCTTTTATATTTGAAAAGGTGTGATTGAC	1902
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QY	1903	GTTAACGGTTTCCACGCTTTTGGCGCATCTCGGAGAACGGTATTGACCTTTCTGGGCG	1962
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QY	2083	GTATTTGGGCGGCAAAAGATGACAGGAGG	2113
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LOCUS	Sequence 112 from Patent WO0066791.		
DEFINITION	AX044033		
ACCESSION	AX044033.1	GI:11342917	
VERSION			
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SOURCE	Neisseria meningitidis		
ORGANISM	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.		
REFERENCE	1		
AUTHORS	Pizza, M., Hickey, E., Peterson, J., Tettelin, H., Venter, J. C., Maignani, V., Galeotti, C., Mora, M., Ratti, G., Scarselli, M., Scarlatto, V., Rappuoli, R., Frazer, C. M. and Grandi, G.		
TITLE	Neisseria genomic sequences and methods of their use		
JOURNAL	Patent: WO 0066791-A. 112 09-NOV-2000;		
FEATURES	CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)		
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QY	121	TTCAAGTCTAGGACGTTTCCACATTCGCTTCCGCGGTCTTCCGTAGAAACACCGCG	180
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QY	181	GTCAACGACCCGCGGTGTTGCGGCAATGCGGCTGTTGAGCGGAATTTTGCACTTCT	240
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QY	241	GATTAAGATGCAATGATTTTCCAAATAGCAACAGCAGAGAAAGCTGTCGTTTAAA	300
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QY	361	AAATTCGTCACCAAAATCTTACGGCAAGCATTCACATCGGAAAGAAATTAATAA	420
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DEFINITION	complete cds.				
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VERSION	1	(bases 1 to 2277)			
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SOURCE	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
ORGANISM	Neisseria meningitidis				
REFERENCE	1 (bases 1 to 2277)				
AUTHORS	Petersson, A., Prinz, T., Umar, A., van der Biesen, J. and Tomassen, J.				
TITLE	Molecular characterization of LbpB, the second lactoferrin-binding protein of Neisseria meningitidis				
JOURNAL	Mol. Microbiol. 27 (3), 599-610 (1998)				
MEDLINE	98149315				
PUBLISHED	1998				
REFERENCE	2 (bases 1 to 2277)				
AUTHORS	Petersson, A., Prinz, T., Umar, A., van der Biesen, J. and Tomassen, J.				
TITLE	Direct Submission				
JOURNAL	Submitted (04-SEP-1997) Department of Molecular Cell Biology, Utrecht University, Padualaan 8, Utrecht 3584 CH, The Netherlands				
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Matches 1672;	Conservative	0;	Mismatches 373;	Indels 72;	Gaps 8;
Qy	1	ATGTGTAACCGCAATTATGCGCGCATTCCTTGTGTCCTTACTTTTGGCATCTTGATC	60		
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Qy	61	GCGCGCAATTTCGGCGTGCAGCTGTGTTCGAATCAACGCCGACCGGTACCCGTCAC	120		
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QY	301	GAGGAAGATPCTTGTGTTTATACGGTTCGAAAGATCAACGTCAGCAGCTTAAGAT	360
Db	400	GAAGTGATGTTCTGTTTATACGGTTCGAAAGATCAACGTCAGCAGCTTAAGAGC	459
QY	361	AAATTTGTCACCAATCTTACGCGAGCATACCATCGGAAAGAAAAATAAAAA	420
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QY	421	TATGATTATAAATTTGTAGATGACAGTTATGTATATCTAAGACGGAAGATGAAT	480
Db	520	TATGATTATAAATTTGTAGATGACAGTTATGTATATCTAAGACGGAAGATGAAT	576
QY	481	GAGTGGACTTCAATTTAAGCAGTCTACCAACCGGTTTGGTTATGACGGTTTGTATAT	540
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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 Pettersson-Fernholm, A.M. and Tommaassen, J.P.
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Query Match 61.0%; Score 1296.2; DB 6; Length 2277;
 Best Local Similarity 79.0%; Pred. No. 3.8e-261;
 Matches 1672; Conservative 0; Mismatches 373; Indels 72; Gaps 8;

QY	1	ATGTGTTAAACCGAATTATGGCGGCAATGTCTTGTTCGCCCTACTTTTGGCATCTTGGCATC	60
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QY	181	GTCAACCGACCCCGCGTGTGGTGGCAATGCGCGTGTGTGAGACGGAATATTGCAACTTCT	240
Db	280	GTCAA CGGCGCCCGCGTGTGGTGGCAATGCGCGTGTGTGAGACGGAATATTGCAACTTCT	339
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QY	301	GAGGAAGATATCTGTGTTTTATACGGTTTCCAAAAAGATCAACGTCAGCAGCTTAAAGAT	360
Db	400	GAAGGTGATGTTCTGTTTTATACGGTTTCAAAAGGAATAAATCTTCAACACTTAAAGC	459
QY	361	AAAAATTCGTCACCAATCTTACGGCAGCAATTCACCATCGAAAAAGAAAAATAAAAA	420
Db	460	GAATTCATAAAGCTGATTCGATATAGAAATTTAGACATCAGAAAAAGGAATAAAAA	519
QY	421	TATGATTATAAATTTGTAGATGCAGGTTATGTTATATCTAAAGACGGAAGATGAAT	480
Db	520	TATGATTATAAATTTGTAGATGCAGGTTATGTTATATCTAAAGACGGAAGATGAAT	576
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Thu Aug 26 10:18:19 2004

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Db 1951 GCGACAGCGCGCACTCGGGATGACGGCATCGACCTTTCGGGACGGTTTCGACCAACCG 2010
QY 1978 AAGAACTTCAAAGCCGACAATCTTCTGTAAACAGCGCGCTTTTATGCGCCCGCAGGGGCA 2037
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Search completed: August 24, 2004, 23:48:01
Job time : 7978.58 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 08:48:44 ; Search time 719.611 Seconds
(without alignments)
12538.967 Million cell updates/sec

Title: US-10-735-098-9
Perfect score: 2124
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : N_Geneseq_29Jan04.*
- 1: Geneseqn1980s.*
 - 2: Geneseqn1990s.*
 - 3: Geneseqn2000s.*
 - 4: Geneseqn2001as.*
 - 5: Geneseqn2001bs.*
 - 6: Geneseqn2002s.*
 - 7: Geneseqn2003as.*
 - 8: Geneseqn2003bs.*
 - 9: Geneseqn2003cs.*
 - 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2124	100.0	2124	2	AAX23323 N. mening
2	1562.4	73.6	2169	2	AAX23320 N. mening
3	1516.8	71.4	2226	7	ACA41945 Prokaryot
4	1499.8	70.6	2226	2	AAX23321 N. mening
5	1375.4	64.8	110000	3	Continuation (2 of
6	1375.4	64.8	349980	3	Aaf21611 Neisseria
7	1296.2	61.0	2277	2	AAX23319 N. mening
8	1291.8	60.8	2262	2	AAX23322 N. mening
9	937.4	23.4	14652	3	AA81482 N. mening
10	497.6	23.4	1000	6	AA91389 N. mening
11	497.6	23.4	1000	6	ABK37769 DNA seque
12	428.8	20.2	707	3	AAA81815 N. mening
13	104.6	4.9	3300	6	ABS67377 Neisseria
14	98.2	4.6	708	5	AAS69547 DNA encod
15	96.8	4.6	801	5	AAS75461 DNA encod
16	95.6	4.5	2334	5	AAS90729 DNA encod
17	95.6	4.5	400	5	AAS75460 DNA encod
18	95	4.5	963	5	AAS68580 DNA encod
19	94.4	4.4	49999	2	AAZ23896 Murine IO
20	94.4	4.4	49999	2	AAZ23891 Murine LO
21	94.2	4.4	453	5	AAS92079 DNA encod
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C 25	93.8	4.4	305	4	ABA66871	Aba66871 Human foe
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C 27	93.8	4.4	305	4	ABA48950	Aba48950 Human bre
C 28	93.8	4.4	305	4	ABA33942	Aba33942 Probe #12
C 29	93.8	4.4	305	4	AAK41027	Aak41027 Human bon
C 30	93.8	4.4	305	4	AAK15306	Aak15306 Human bon
C 31	93.8	4.4	305	4	ABS40624	Abs40624 Human liv
C 32	93.8	4.4	305	5	AAI07480	Aai07480 Probe #74
C 33	93.8	4.4	305	6	ABS15007	Abs15007 Human gen
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C 35	93.8	4.4	496	4	AAI12609	Aai12609 Probe #25
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C 42	93.8	4.4	496	4	ABS27626	Abs27626 Human liv
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C 44	93.8	4.4	496	6	ABS02506	Abs02506 Human gen
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ALIGNMENTS

RESULT 1
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ID AAX23323 standard; cDNA; 2124 BP.
XX
AC AAX23323;
DT 11-JUN-1999 (first entry)
DE N. meningitidis strain 881607 LbpB cDNA.
XX
KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;
meningitis; diagnosis; treatment; ds.
XX
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FH Key Location/Qualifiers
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FT FT /product= "LbpB"
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PN WO9909176-A1.
XX
PD 25-FEB-1999.
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PF 10-AUG-1998; 98WO-EF005117.
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PR 15-AUG-1997; 97GB-00017423.
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PR 05-FEB-1998; 98GB-00002544.
XX
XX (UYUT-) RIJKSUNIV UTRECHT.
XX (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.
XX
XX Pettersson-Fernholm AM, Tommassen JPM;
XX
XX WPI; 1999-190165/16.
XX
XX P-PSDB; AAW93496.
XX
XX New lactoferrin-binding protein B polynucleotides - obtained from
XX Neisseria meningitidis, used to develop products for the diagnosis,
XX prevention and treatment of neisserial disease, e.g. meningitis.
XX
XX Claim 2; Page 105-109; 116pp; English.
XX
XX This invention describes novel lactoferrin-binding protein B (LbpB)
XX strains of Neisseria meningitidis. The products of this invention can be
XX used for vaccinating humans against neisserial disease e.g. meningitis.

APP/CA/B

CC	Antibodies raised against the proteins of the invention can be used for									
CC	diagnosing or treating neisserial disease in humans. The LbpB									
CC	polypeptides can also be used for identifying compounds which inhibit the									
CC	polypeptides									
XX										
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QY	301	GAGGAAGATATCCTGTTTATACCGTTTCCAAAAGATCAACGCTGACGAGCTTAAAGAT	360							
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QY	361	AAAATTCGTCAACCAATTCCTACGGCAAGCATTCACATCGGAAAGAAAATAAAAA	420							
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DB	421	TATGATTAATAATTTGTAGATGCAGGTTATCTATATATACTAAAGACGAAAGATGAAT	480							
QY	481	GAGTGACCTCAAAATPACAGCAGTCTCAACCGGTTTGGTTATGACGGTTTGTATAT	540							
DB	481	GAGTGACCTCAAAATPACAGCAGTCTCAACCGGTTTGGTTATGACGGTTTGTATAT	540							
QY	541	TATTCGGGAGAACATCTTTCGCAATCTTTTACCGAGCGCGGAAACGGTGAATATTCGGG	600							
DB	541	TATTCGGGAGAACATCTTTCGCAATCTTTTACCGAGCGCGGAAACGGTGAATATTCGGG	600							
QY	601	AACCTGCAATATATGACCGATGCCATAGTCAATCGAACAGAAAGCAGGAGATCTTAGC	660							
DB	601	AACCTGCAATATATGACCGATGCCATAGTCAATCGAACAGAAAGCAGGAGATCTTAGC	660							
QY	661	GAAAGATTGGGTTATATCGTTTATACGGTCAAAATGTCGGAGCACTTCTTATGCTGCG	720							
DB	661	GAAAGATTGGGTTATATCGTTTATACGGTCAAAATGTCGGAGCACTTCTTATGCTGCG	720							
QY	721	ACTGCCGACGACCGGAGGAAACAACTCTCGCAATATACGGTTAAATTCGACCAAAAA	780							
DB	721	ACTGCCGACGACCGGAGGAAACAACTCTCGCAATATACGGTTAAATTCGACCAAAAA	780							
QY	781	ACTCTGAATGGCAAGCTGATTAATAATCAGTATGTGCAAAAGAGAGATGATCTTAAAA	840							
DB	781	ACTCTGAATGGCAAGCTGATTAATAATCAGTATGTGCAAAAGAGAGATGATCTTAAAA	840							
QY	841	CCACTGACCAATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTAAC	900							
DB	841	CCACTGACCAATTAACGATTAACGATTAACGATTAACGATTAACGATTAACGATTAAC	900							
QY	901	AAAGTTAACACAGAGGTGAAGACGAATCACGCTGATTAAGAAATATTTGTTTTCATACC	960							

DB	901	AAAAGTTAACACAGAGGTGAAGACGAATCAAGCTGATAAAGAAATATTTGTTTTCATACC	960
QY	961	GATGCCGATCAGCGGCTTGAGGGCGGTTTTCGCGCATAGAGGGGAGAGCTTGCCGGA	1020
DB	961	GATGCCGATCAGCGGCTTGAGGGCGGTTTTCGCGCATAGAGGGGAGAGCTTGCCGGA	1020
QY	1021	CGGTTTATCAGCAACGACAGCGTATTCGGCGTGTTCGAGGCAACAAAAACAGAG	1080
DB	1021	CGGTTTATCAGCAACGACAGCGTATTCGGCGTGTTCGAGGCAACAAAAACAGAG	1080
QY	1081	ACAGCAACGACATCAGATACAAATCCCTGCCCTCTCGGAACACACCAAAATCTTG	1140
DB	1081	ACAGCAACGACATCAGATACAAATCCCTGCCCTCTCGGAACACACCAAAATCTTG	1140
QY	1141	GATTTCTTAAATTTCCGTTTGACGAGCAAGTGTGAAATCCCGACCGTTTGAGGTT	1200
DB	1141	GATTTCTTAAATTTCCGTTTGACGAGCAAGTGTGAAATCCCGACCGTTTGAGGTT	1200
QY	1201	TCCACTATGCCCGATTTTGGTTCATCCCGACAAATCTTCTGTGGAAGGGCGTGAATTCCT	1260
DB	1201	TCCACTATGCCCGATTTTGGTTCATCCCGACAAATCTTCTGTGGAAGGGCGTGAATTCCT	1260
QY	1261	TTGGTAAACAAAGAACAAACCATCTTCCGACGCGCAGGAAATGACCGTCCGTCGT	1320
DB	1261	TTGGTAAACAAAGAACAAACCATCTTCCGACGCGCAGGAAATGACCGTCCGTCGT	1320
QY	1321	TGTTGCGACTTTTTCGCTATGTGAAATCTCGGACGATTAATAACCGACGCGCCGCTC	1380
DB	1321	TGTTGCGACTTTTTCGCTATGTGAAATCTCGGACGATTAATAACCGACGCGCCGCTC	1380
QY	1381	CAACCGAAGGGCGAGGATGAAGAGGGGAGAGAGGGGTGTAGGGTTGTATACCGTAAA	1440
DB	1381	CAACCGAAGGGCGAGGATGAAGAGGGGAGAGAGGGGTGTAGGGTTGTATACCGTAAA	1440
QY	1441	GAAAGCGAAGCGAATTCGCGATCAAGAAACCGCAGACGAAAGTCTGTAAGATGAA	1500
DB	1441	GAAAGCGAAGCGAATTCGCGATCAAGAAACCGCAGACGAAAGTCTGTAAGATGAA	1500
QY	1501	GACGAAGATGAAGACGAAGAAATCGAAGAAAGAACTTGAAGAAAGCTGAAGAGAA	1560
DB	1501	GACGAAGATGAAGACGAAGAAATCGAAGAAAGAACTTGAAGAAAGCTGAAGAGAA	1560
QY	1561	GAAACCGAAGAAAGATTCGCGGACGAAGAGCGGCTTTCAGGAGAGCTTCCTGCC	1620
DB	1561	GAAACCGAAGAAAGATTCGCGGACGAAGAGCGGCTTTCAGGAGAGCTTCCTGCC	1620
QY	1621	ACTCCGAGAGCTTAAAGCGAGGACATCGACTTTTCTGAAAGGTATTCGACGCGG	1680
DB	1621	ACTCCGAGAGCTTAAAGCGAGGACATCGACTTTTCTGAAAGGTATTCGACGCGG	1680
QY	1681	GAAACCGAAGAAAGATTCGCGGACGAAGAGCGGCTTTCAGGAGAGCTTCCTGCC	1740
DB	1681	GAAACCGAAGAAAGATTCGCGGACGAAGAGCGGCTTTCAGGAGAGCTTCCTGCC	1740
QY	1741	GCGGTATCGGATAGTGTCTCATTAAGAGATAGCTATCGGATCAAGGGGCAAAA	1800
DB	1741	GCGGTATCGGATAGTGTCTCATTAAGAGATAGCTATCGGATCAAGGGGCAAAA	1800
QY	1801	GCAGAAATTTACCGTTGATTTTGAAGCGAAGCGGCTTTCGGAATGTGTGAAGAAAAAT	1860
DB	1801	GCAGAAATTTACCGTTGATTTTGAAGCGAAGCGGCTTTCGGAATGTGTGAAGAAAAAT	1860
QY	1861	GATACAAACCCCGCTTTTATATTTGAAAAAGGTGTGATGACGGTAAACGGTTCCAGCT	1920
DB	1861	GATACAAACCCCGCTTTTATATTTGAAAAAGGTGTGATGACGGTAAACGGTTCCAGCT	1920
QY	1921	TTGGCGCATATCTCGGAGAACGGTATTCGCTTTCGCGAGGGTTCGACTTAACCCGAG	1980
DB	1921	TTGGCGCATATCTCGGAGAACGGTATTCGCTTTCGCGAGGGTTCGACTTAACCCGAG	1980
QY	1981	AACCTTCAAGCGCAATCTTCTTGTAAACAGCGCGCTTTTATGGCCCGCAGAGCA	2040
DB	1981	AACCTTCAAGCGCAATCTTCTTGTAAACAGCGCGCTTTTATGGCCCGCAGAGCA	2040

QY 2041 TTGGCGGTATATATCGACAGCGACCGGAAATTCGTTGGGTATTTGGGCGGAAAAA 2100
 Db |||||
 2041 TTGGCGGTATATATCGACAGCGACCGGAAATTCGTTGGGTATTTGGGCGGAAAAA 2100
 QY 2101 GATGACAAAGGAGGCAACACGATGA 2124
 Db |||||
 2101 GATGACAAAGGAGGCAACACGATGA 2124

RESULT 2

AAX23320

ID AAX23320 standard; cDNA; 2169 BP.

XX AC AAX23320;

XX DT 11-JUN-1999 (first entry)

XX DE N. meningitidis strain M981 LbpB cDNA.

XX KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;

XX KW meningitis; diagnosis; treatment; ds.

XX OS Neisseria meningitidis.

XX FH Key

XX FT CDS

XX FT Location/Qualifiers

XX FT 1. 2169

XX FT /*tag= a

XX FT /product= "LbpB"

XX PN WO9909176-A1.

XX PD 25-FEB-1999.

XX PF 10-AUG-1998; 98WO-EP005117.

XX PR 15-AUG-1997; 97GB-00017423.

XX PR 05-FEB-1998; 98GB-00002544.

XX XX

XX PA (UYUT-) RIJKSUNIV UTRECHT.

XX PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.

XX PI Pettersson-Fernholm AM, Tommassen JPM;

XX PI WPI; 1999-190165/16.

XX DR P-PSDB; AAW93493.

XX XX

XX PT New lactoferrin-binding protein B polynucleotides - obtained from

XX PT Neisseria meningitidis, used to develop products for the diagnosis,

XX PT prevention and treatment of neisserial disease, e.g. meningitis.

XX XX

XX PS Claim 2; Page 82-86; 116pp; English.

XX CC This invention describes novel lactoferrin-binding protein B (LbpB)

XX CC strains of Neisseria meningitidis. The products of this invention can be

XX CC used for vaccinating humans against neisserial disease e.g. meningitis.

XX CC Antibodies raised against the proteins of the invention can be used for

XX CC diagnosing or treating neisserial disease in humans. The LbpB

XX CC polypeptides can also be used for identifying compounds which inhibit the

XX CC polypeptides

XX XX

XX SQ Sequence 2169 BP; 675 A; 457 C; 550 G; 487 T; 0 U; 0 Other;

XX

XX Query Match

XX Best Local Similarity 73.6%; Score 1562.4; DB 2; Length 2169;

XX Matches 1835; Conservative 0; Mismatches 286; Indels 51; Gaps 5;

XX

XX QY 1 ATGTGTAACCGAATTATGCGGCATGCTGTGTCCTTACTTTGGCATCTTCATC 60

XX Db 1 ATGTGTAACCGAATTATGCGGCATGCTGTGTCCTTACTTTGGCATCTTCATC 60

XX

XX QY 61 GCGCGCAATTCGGGTGAGCGCTGTGTGGAATCAACCGCACCGGTACCCCGTCACT 120

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Db 61 GCGCGCAATTCGGGTGAGCGCTGTGTGGAATCAACCGCACCGGTACCCCGTCACT 120
 QY 121 TTCAAGTCTAAGGACGCTTCCCACTTCGCCCTCTCGCCGGTCTTCGGTAGAAACACACGCG 180
 Db 121 TTCAAGTCTAAGGACGCTTCCCACTTCGCCCTCTCGCCGGTCTTCGGTAGAAACACACGCG 180
 QY 181 GTCAACCGACCCCGCTTGGTGGGCAATCGCGCTGTGAGACGGAATATTGCACTTCT 240
 Db 181 GTCAACCGACCCCGCTTGGTGGGCAATCGCGCTGTGAGACGGAATATTGCTTTTCAT 240
 QY 241 GATAAGGATGGCAATGATTTTCCAAATAGCAAAACAAGCAGACGAAAGCTGTCTTTAAA 300
 Db 241 CGTGAAGATGGCACGCGCAATTCGGATAGCAAAACAAGCAGACGAAAGCTGTCTTTAAA 300
 QY 301 GAGGAAGATATCTCTGTTTATACGGTTCCTCAAAAGATCAACGTGACGAGCTTAAAGAT 360
 Db 301 GAAGGTGATGTTCTGTTTATACGGTTCCTCAAAAGATCAACGTGACGAGCTTAAAGAT 360
 QY 361 AAAATTCGTCACCAATCTTACCGCAAGCATTTACCAATCGGATCGGAAAGCTTAAAGAT 420
 Db 361 GAAATTCATAAAGCTAATCTTACCGCAAGCATTTACCAATCGGATCGGAAAGCTTAAAGAT 420
 QY 421 TATGATTATAAATTTAGATGAGGATTAATGATATATCTTAAAGACGAAAGCTTAAAGAT 480
 Db 421 TATAATTATCGGTTTGTAGTCCGGTATGTTGTTTACTTAAAGACGAAAGCTTAAAGAT 480
 QY 481 GAGTGGACTTCAAAATACAGCAGTCTACCAACCGTTCACCAACCGTTCGAAATTTGATAT 540
 Db 481 GAGAAACATCGGATGAAAGCAGTTTCTAATCGTTTAGGCTATGACGCTTGTATAT 540
 QY 541 TATCCGGAGAACATCTTTCGCAATCTTACCGACGCGGGAACGCTGAAATTTCCGCG 600
 Db 541 TATCTCGGAGAACATCTTTCGCAATCTTACCGACGCGGGAACGCTGAAATTTCCGCG 600
 QY 601 AACTGGCAATATATGACCGATGCCATACGTTCATCGAGAGGATGATCTTAAAGAT 660
 Db 601 AACTGGCAATATATGACCGATGCCATACGTTCATCGAGAGGATGATCTTAAAGAT 660
 QY 661 GAAATTTGGCTTATATCGTTTATACGGTCAAAATGTCGGAGCAATCTTATGCTCGG 720
 Db 658 GTGGATTTGGGTTATACCAATATTTATGTTGTAATGAAATTTGGGCGACGCTTCTTATGAGCT 717
 QY 721 ACTGCGACGACCGGAGGAGGAAACATCTTCCGCAATATACGTTTAAATTTTCGACCAAAA 780
 Db 718 AGGATGCGGATGCGCGGGAAGAAACATCTTCCGCAATATACGTTTAAATTTTCGACCAAAA 777
 QY 781 ACTCTGATGCAAGCTGATTAATAAATGATGATGCAAAAGAGAGATGATCTTAAAGAT 840
 Db 778 AACCTGGAAGTAAAGTTGATTAATAAATGATGATGCAAAAGAGAGATGATCTTAAAGAT 837
 QY 841 CCATGACCAATTTACGACATTTACTGCAAAATTTGACGCGCAACCGCTTTACCGGAGTGCC 900
 Db 838 CCATGACCAATTTACGACATTTACTGCAAAATTTGACGCGCAACCGCTTTACCGGAGTGCC 897
 QY 901 AAAGTTAAACAGAGGTGAAGACGATCAGCTGATTAAGAAATTTGTTTTCATACC 960
 Db 898 AAAGTTAGCACCGGATGAAGACGACGCTGATTAAGAAATTTGTTTTCATACC 957
 QY 961 GATGCGATCAGCGCTTGGGCGGTTTTCGCGGATAAGGGGGAAGAGCTTTCGCGGA 1020
 Db 958 GATGCGGATCAGCGCTTGGGCGGTTTTCGCGGATAAGGGGGAAGAGCTTTCGCGGA 1017
 QY 1021 CGGTTTATCAGCAACGACACGCTTATTCGGGCTGTTTCGAGGCAACCAAAAAACAGAG 1080
 Db 1018 CGGTTTATCAGTAAACGACACGCTTATTCGGGCTGTTTCGAGGCAACCAAAAAACAGAG 1077
 QY 1081 ACAGCAACGCTATCAGATACAAATCTGCGCTGCGCTCTGGAAGAAACACACCAAAATCTTG 1140
 Db 1078 ACAGCAACGCTATCAGATACAAATCTGCGCTGCGCTCTGGAAGAAACACACCAAAATCTTG 1137
 QY 1141 GATTTCTTAAATTTTCGTTGACGAGGCAAGTGGTGAAGATCCCCCGACCGTTTTCAGGTT 1200
 Db 1138 GATTTCTTAAATTTTCGTTGACGAGGCAAGTGGTGAAGATCCCCCGACCGTTTTCAGGTT 1197

1201 TCCACTATGCCGATTTTGGTGTATCCCGACAAATCTTGTGCGAAGGCGTGAATTCCT 1260
1198 TCCACTATGCCGATTTTGGTGTATCCCGACAAATCTTGTGCGAAGGCGTGAATTCCT 1257
1261 TTGGTAACAAAGAACAAATCATCATGATCTTGGCGACGCGAGGAAATGACCGTCCGTC 1320
1258 TTGGTTAGCAAGAAACCATCGATCTGCCACGCGGAGGAAATGACCATCCGTCGCT 1317
1321 TGTTCGACATTTTGTGACTATGTGAACTCCGACGCGATATAAACCAGACGCCCGCCGTC 1380
1318 TGTTCGACATTTTGTGACTATGTGAACTCCGACGCGATATAAACCAGACGCCCGCCGTC 1377
1381 CAACCGAAGCGCGAGGATGAAGAGGCGGACGAGAGGCTGTAGCGTGTATTAACGTA 1440
1378 AAACCGAAGCGCGAGGATGAAGAGGCTGTAGCGTGTATTAACGTAAGGAGGAGAC 1437
1441 GAAA---GCGAAGCAGAAATCGCGATGAAGAGCACCAGGAG----- 1481
1438 GAAATTTCCGAAGATGATTAACGCGGAGATGAAGTCAACGAGAGAGGAGCTGAAGAA 1497
1482 --CGAAGTCGTAGAAGATCAAGACGAGATGAAGACGAGAGGAAATCGAA-----GAA 1533
1498 ACCGAGAGAACTGATGAGACGAGAGGAGAACCCGAGAGAACTGAAGAAACTGAA 1557
1534 GAACCTGAAGAGAGCTGAAGAGAGAGAACCCGAGAGAGATTCGCGGACGAGAGGCG 1593
1558 GAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAGAACTGAAG 1617
1594 AACGCGGTTCAAGGAGCATCTGCCCTCCGAGGCTCTAAAGGAGGAGGACATCGAC 1653
1618 AACGCGGTTCAAGGAGCATCTGCCCTCCGAGGCTCTAAAGGAGGAGGACATCGAC 1677
1654 CTTTTCCTGAAAGGATTCGCGAGCGGAGGAGGAGGATTCGCGAGGAGGAGGAGG 1713
1678 CTTTTCCTGAAAGGATTCGCGAGCGGAGGAGGAGGATTCGCGAGGAGGAGGAGG 1737
1714 TATACCGGCACTTGGAGAGCGGTATCGCGGTATCGGATA----- 1753
1738 TATACCGGCACTTGGAGAGCGGTATCGCGGTATCGGATAAGAGGCGGAGGAGGAGT 1797
1754 -GTGGTACCTCCATTCAGAGGATAGCTATGCGAATCAAGGGGCAAGAGGAGGAGT 1812
1798 GGCATACGCTCCATTCAGAGGATAGCTATGCGAATCAAGGGGCAAGAGGAGGAGT 1857
1813 GTTGATTTGGAAGCAGAGCGGTGTCGCGAATGCTGACGAGGAGGAGGAGGAGGAG 1872
1858 GTTGATTTGTCGAGGAGTGCCTTCAGGTAGTTCAGAGGAGGAGGAGGAGGAGGAG 1917
1873 GCTTTTATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1932
1918 GCTTTTATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1977
1933 CGGAGAGAGGATTCGACCTTTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1992
1978 CGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2037
1993 GACAACTCTTCTTAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2052
2038 AGTAATCTCTCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2097
2053 ATTATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2112
2098 ATTATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2157
2113 GCAACAGCATGA 2124
2158 GTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG

RESULT 3
ACA41945
ID ACA41945 standard; DNA; 2226 BP.

ACA41945;
19-JUN-2003 (first entry)
Prokaryotic essential gene #23602.
Antisense; ds; prokaryotic essential gene; cell proliferation;
drug design; gene.
Neisseria meningitidis.
WO200277183-A2.
03-OCT-2002.
21-MAR-2002; 2002WO-US009107.
21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
(ELIT-) ELITRA PHARM INC.
Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
WPI; 2003-029926/02.
P-PSDB; ABU38075.
New antisense nucleic acids, useful for identifying proteins or screening
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
Claim 14; SEQ ID NO 29815; 1766pp; English.
The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
nucleic acid; (2) a host cell containing the vector; (3) an isolated
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
proliferation or the activity of a gene in an operon required for
proliferation; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
pathway in which a proliferation-required gene or its gene product lies
or a gene on which the test compound that inhibits proliferation of an
organism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the gene
product is overexpressed or underexpressed; (12) determining the extent
to which each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
proliferation of an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
for cellular proliferation to isolate candidate molecules for rational
drug discovery programs, or for screening homologous nucleic acids
required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
K. pneumoniae or *P. aeruginosa*. The present sequence is one of the target
prokaryotic essential genes. Note: The sequence data for this patent did
not form part of the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

Sequence 2226 BP; 701 A; 466 C; 566 G; 493 T; 0 U; 0 Other;
Query Match 71.4%; Score 1516.8; DB 7; Length 2226;

Best Local Similarity 83.3%; Pred. No. 0; Matches 1792; Conservative 0; Mismatches 307; Indels 51; Gaps 4;	
QY	1 ATGTGTAACCCGAATTAATCGCGCAATGCTGCTGTTGCCCTTACCTTTGCGCACTTTGCAATC 60
Db	1 ATGTGTAACCCGAATTAATCGCGCAATGCTGCTGTTGCCCTTACCTTTGCGCACTTTGCAATC 60
QY	61 GGCGGCAATTTGGCGGTGAGCGTGTGTCGAATCAACGCCGACCGCGTACCGCGTCACT 120
Db	61 GGCGGCAATTTGGCGGTGAGCGTGTGTCGAATCAACGCCGACCGCGTACCGCGTCACT 120
QY	121 TTCAAGTCTAAGAGAGTTCCTCCACTTCGCGCTCTGCGGGTCTTGGGTAGAAACACCGCG 180
Db	121 TTCAAGTCTAAGAGAGTTCCTCCACTTCGCGCTCTGCGGGTCTTGGGTAGAAACACCGCG 180
QY	181 GTCAACCCGACCCCGCTTGGTGGCGCAATGCGGCTGTTGACCGGAATATGTCGAATTTCT 240
Db	181 GTCAACCCGACCCCGCTTGGTGGCGCAATGCGGCTGTTGACCGGAATATGTCGAATTTCT 240
QY	241 GATAAGGATGGCAATGATTTTCCAAATAGCAAAACAAGCAGAGAAAAGCTGTGCTTTAAA 300
Db	241 CGTGAAGATGGCAGCGCAATTCGCGATAGCAAAACAAGCAGAGAAAAGCTGTGCTTTAAA 300
QY	301 GAGGAAGATATCTCTGTTTTATACGGTTCCAAAAAGATCAAAGTCAAGAGCTTTAAGAT 360
Db	301 GAAAGTGAATGTTCTGTTTTATACGGTTCCAAAAAGATCAAAGTCAAGAGCTTTAAGAT 360
QY	361 AAAATTCGTCAACCAAAATCTTACCGCAAGCAATACCACATCGGAAAGAAAATRAAAA 420
Db	361 AAAATTCATCAACCAATCTTAAATGTAGAAATAGGACATCAGAAATGAAAATRAAAA 420
QY	421 TATGATTAATAATTTGTAGATGCAAGTTATGTATATACTAAAGACGGAAGAGTGAAT 480
Db	421 TATGGTTATGAATTTGTAGATGCAAGTTATGTATATACTAAAGAGGAAAGATGAAT 480
QY	481 GAGTGGACTTCAAATTAACAGCACTTACCAAACGGTTTGGTTATGACGGTTTGGPATAT 540
Db	481 GAGTGGACTTCAAATTAACAGCACTTACCAAACGGTTTGGTTATGACGGTTTGGPATAT 540
QY	541 TATTCCGGAGAACATCTCTCGCAATCTTACCAGCGCGGAGCGGTGAATATTTCCGCG 600
Db	541 TATTCCGGAGAACATCTCTCGCAATCTTACCAGCGCGGAGCGGTGAATATTTCCGCG 600
QY	601 AACTGGCAATATATGACCGATGCGATACGTCGAACAGGAAAAGCAGAGATCCTAGC 660
Db	601 AACTGGCAATATATGACCGATGCGATACGTCGAACAGGAAAAGCAGAGATCCTAGC 660
QY	661 GAAGATTTGGTTATATCGTTTATACGTTCAAAATGTGCGAGCAACTTCTTATGCTGG 720
Db	661 GAAGATTTGGTTATATCGTTTATACGTTCAAAATGTGCGAGCAACTTCTTATGCTGG 720
QY	721 ACTGCCGACACCGGGAGGAAAACATCTCGCGAATATACGTTTAAATTTGACACCAAAA 780
Db	721 ACTGCCGACACCGAGGGAAAACATCTCGCGAATATACGTTTAAATTTGAGTAAGAAA 780
QY	781 ACTCTGAATGGCAAGCTGATTAATAATCATGATGTGCAAAAGAGAGATGATCTAAAAAA 840
Db	781 ACTTTGACGGTAAATTAATTAATAATCATGATGTGCAAAAGAAACCGATGAAAGAAA 840
QY	841 CCAGTCAACATTTACACATTAAGTCAAAATTTGAGCGGCAACCGTTTACCGGAGTGCC 900
Db	841 CCAGTCAACATTTACACATTAAGTCAAAATTTGAGCGGCAACCGTTTACCGGAGTGCC 900
QY	901 AAGATTAAACAGAGGTGAAGACGAATCAAGCTGATAAAGATAATTTGTTTTTCCATACC 960
Db	901 AAGATTAAACAGAGGTGAAGACGAACACGCTGATAAGAGCAATTTGTTTTTCCATACC 960
QY	961 GATGCCGATCAGCGCTTGAGGGCGGTTTTTTTCGCGGATAAGGGGGAAGACTTTGCCGGA 1020
Db	961 GATGCCGATCAGCGCTTGAGGGCGGTTTTTTTCGCGGATAAGGGGGAAGACTTTGCCGGA 1020
QY	1021 CGGTTTTATCAGCAACGACAAACAGCTTATTCGCGGTGTTTCGAGGCAACAAAAACAGAG 1080
Db	1021 CGGTTTTATCAGCAACGACAAACAGCTTATTCGCGGTGTTTCGAGGCAACAAAAACAGAG 1080

1315 CGTCTGTTGCGACTTTTGGACCTATGTGAATCTCGACGATATAAAACCGACGCC 1374
1318 CGTCTGTTGCGACTTTTGGACCTATGTGAATCTCGACGATATAAAACCGACGCC 1377
1375 GCGCTCAACCGAAGCGCGAGTGAAGAGGGGACGAAGAGGTGTAGCGCTTGTATAAC 1434
1378 GCAAGTAAACCAAGGCGAAGATAAAGGAAGATGAAGAGGATACAGCGTGTGTAA 1437
1435 GGTAAAGAAAGCGAAGCAAGCAATCGCGATGAAGAAAGACCGGAGACGAAGTGTAGAA 1494
1438 GACGAAGAGGACCGAAGATGAAGCGCGAAGAGGAGCGAAGAGCGGAGCAATC 1497
1495 GATGAAGACGAAGATGAAGCAAGCAAGAAATCGAAGAA-----GNAACGTGAA 1542
1498 GCGATGAAGAGGAGGTGCGGAGAGCAAGCGCGAGAAACGAAGCGCGGAGAGAC 1557
1543 GAAGAAGCTGAAGAGGAAGAACCGGAAGAAATTCGCGGAGAAAGGCAAGCGCGT 1602
1558 GAAGCTGAAGAACCTGAAGAACCGGAAGAAATTCGCGGAGAGGCGCGGTGTGT 1617
1603 TCAGGCGAGCATCTGCGCCACTCGGAGGCTCTAAGGCGAGGACATCGACCTTTTCTG 1662
1618 TCAGGCGCATCTGCGCCACTCGGAGGCTCTAAGGCGAGGACATCGACCTTTTCTG 1677
1663 AAGGTATCCGACGCGGAGGCGGACATTCGCAAAAGCGGAGCGGCGATATACCGGC 1722
1678 AAGGTATCCGACGCGGAGGCGGACATTCGCAAAAGCGGAGCGGCGATATACCGGC 1737
1723 ACTTGGGAGCGGTATCGGCGTATCGGATGTGTAAGTTCATTCGCAAAAGGATAGCTAT 1782
1738 ACTTGGGAGCGGTATCAGC-----AAACCATTCATGGGACATCAT 1782
1783 GCG---AATCAAGGGGCAAAAGCAGATTTACGGTGTATTCGAAGCGAAGCGGTGCC 1839
1783 GCGATATAAAGCGGCAAAAGCAGATTTACGGTGTATTCGAAGCGAAGCGGTGCC 1842
1840 GGAATGCTGCAGAAAAAATGATACACACCGCTTTTATATTTGAAAAAGGTGTGAT 1899
1843 GGAACGCTGCAGGAGAAAAAGCGGTGTACACCTGCTTTCCATATTTGAAAAAGCGGTGAT 1902
1900 GACGTTAACGTTTCCAGCTTTGCGGATATCTCGGAGAACGCTATTCGCTTCTGGG 1959
1903 GAGGCGAATGTTTCCAGCGACAGCGCGCATCGGATACGCGCATCATCTTTCGGA 1962
1960 CAGGTTTCGACTAACCGGAGACCTTCAAGCGGACAACTCTTCTTTGAACGCGGCTTT 2019
1963 AATGATTCGACTAATCTCCAGGTTTCAAGGCCAATAATCTTCTTTGAACGCGGCTTT 2022
2020 TATGGCCCGCAGCGCGGAGAAATGGGCGGTAAATATTCGACGCGGAGAAATTCGCT 2079
2023 TACGCGCCGCGAGCGGAGGAAATGGGCGGTACTATTTTCAATATGATGGGAAATCTCTT 2082
2080 GCGGTATTTGGGCGGAAAAAGATGACAGAGGC 2114
2083 GGTATAACTGAAGATACGTAATGAAGCTGAAGC 2117

RESULT 5

AA81489_1/c

Continuation (2 of 9) of AA81489 from base 100001 (N. meningitidis partial DNA sequence)
WP Sequence split into 9 fragments LOCUS AA81489 Accession AA81489

WP	Fragment Name	Begin	End
WP	AA81489_0	1	110000
WP	AA81489_1	100001	210000
WP	AA81489_2	200001	310000
WP	AA81489_3	300001	410000
WP	AA81489_4	400001	510000
WP	AA81489_5	500001	610000
WP	AA81489_6	600001	710000
WP	AA81489_7	700001	810000
WP	AA81489_8	800001	837096

Query Match 64.8%; Score 1375.4; DB 3; Length 110000;
Best Local Similarity 80.2%; Pred. No. 0;
Matches 1709; Conservative 0; Mismatches 371; Indels 51; Gaps 6;
QY 1 ATGTGTAACCGAATATATGGCGCATTTGCTTGTGCCCCTACTTTTGGCATCTTGATC 60
Db 64252 ATGTGTAACCGAATATATGGCGCATTTGCTTGTGCCCCTACTTTTGGCATCTTGATC 64193
QY 61 GCGCGCAATTTCCGCGCTGCGACTGTTTGCATCAACGCGGACCGGCTTACCCTGCTCAT 120
Db 64192 GCGCGCAATTTCCGCGCTGCGACTGTTTGCATCAACGCGGACCGGCTTACCCTGCTCAT 64133
QY 121 TTCAAGTCTAAGAGAGCTTCCCACTTCCGCTCTCGCTCGCGGTCTTCGTTAGAAACACCGCG 180
Db 64132 TTCAAGTCTAAGAGAGCTTCCCACTTCCGCTCTCGCTCGCGGTCTTCGTTAGAAACACCGCG 64073
QY 181 GTCAACCGACCGCGCTTGGTTCGCGCAATTCGCGCTGTTGAGACGGAATATTCGAATCTCT 240
Db 64072 GTCAACCGACCGCGCTTGGTTCGCGCAATTCGCGCTGTTGAGACGGAATATTCGAATCTCT 64013
QY 241 GATAAGGATGCAATGATTTTCCAAATAGCAAAACGAGAGAAAGCTGCTGTTTAAA 300
Db 64012 AAGCAAGACGGTACGGAATTTCCGCAAGCATCAGGCGAGAGCATCTGCGCGCTTAAA 63953
QY 301 GAGGAGATATCTCTGTTTATACGGTTTCCAAAGAGATCAACGTCAGCAGCTTAAAGAT 360
Db 63952 GAGGAGATATCTCTGTTTATAGCGGTGCTGAAAGAACAGGCTGACAAACTTTAAAAAG 63893
QY 361 AAAATTCGTAACCAATCTTACGCGCAAGCATTACCATCGGAAAGAAATAAAAA 420
Db 63892 AAAATTCGTAACGAGCATTTCTGATGTGAGGCTTATCATCGAAAGAGAGAGAAAA 63833
QY 421 TATGATTAATAATTTGATAGTCAAGTTATGTAATACTA-----AAGACGGAAGAT 474
Db 63832 TATCAATATCAATTTGTCGCGGCTGATGTGTTTACCGGCGGAGAGAGATAT 63773
QY 475 GAAATTCAGTGCATCTCAAATTTACAGCAGTCTACCAACCGGTTTGTATTGACGTTT 534
Db 63772 GAAAGAGAAAGACTTCTGATGTGTAAGGTTTGTAAACCGATTTAGTTATGACGTTT 63713
QY 535 GTATATTATTCGAGAACATCTCTTCGCAATCTTTACCGAGCGGGAACGTTGAAATAT 594
Db 63712 GTATATTATTCGAGAACATCTCTTCGCAATCTTTACCGAGCGGGAACGTTGCAATAT 63653
QY 595 TCCGCGCAACTGGCAATATATGACGATCCATGCTCATCGAATCGAAGAGAGAGAT 654
Db 63652 TCCGCTAACCTGGCAATATATGACGATCCGCAACGCTCATCGGACAGTAAAGC---GGTT 63596
QY 655 CCTAGCGAAGATTTGGGTTATATCGTTTATTTACGTCMAAATCTCGGAGCAACTTCTAT 714
Db 63595 TCCAGTACCGATTTGGGTTATACCAATATTTGGTAATGAAATGGGGCAACTTCTAT 63536
QY 715 GCTGCGACTGCGGACGACCGGGAGGAAACATCTCTCGCAATATACGTTTAAATTCGAC 774
Db 63535 GAGGCTAGGATGCGCGACGACGAGGAAAGAGCATCTGCGCAATATACGTTTGTATTTGAT 63476
QY 775 CAAAAAATCTGAAATGCGAAGCTGATTTAAATCAGTATGTGCAAAAG-----GA 825
Db 63475 AACAAACCTGAAATGCGAAGCTGATTTAAATCAGTATGTGCAAAATTAAGTAAATCCA 63416
QY 826 GATGATCTTAAAAACCACTGACCATTTTACGACATTTACTGCAAAATTTGACGCGCAACCG 885
Db 63415 AATGAGCCCAAAACCGCTGACCATTTTACGACATTTACGCAACATTTGACGCGCAACCG 63356
QY 886 TTTACCGGAGTGCAGAAAGTTTAAACAGAGGTGAAGACGAATCAGCTGATATAAGATAT 945
Db 63355 TTTACCGGAGTGCAGAAAGTTTAAACAGAGGTGAAGACGAATCAGCTGATATAAGATAT 63296
QY 946 TTGTTTTTCCATACCGATCCGATCAGCGGCTTGAAGGCGGTTTTTTCGGGATTAAGGG 1005
Db 63295 TTGTTTTTCCATACCGATCCGATCAGCGGCTTGAAGGCGGTTTTTTCGGGATTAAGGG 63236
QY 1006 GAAGAGCTTTCGCGGAGCGGTTTATCAGCAACGACACAGGCTATTCGCGGTGTTCCAGGC 1065

62185 ATAACTGAAGTACTGAAATAAAGTTGATG 62155

QY	1066	AAACAAAAACAGACAGCAAAACGATCAGATACAAATCCTCGCTCGGTGTGAAAA	1125
Db	63175	AAACAAAAACAGACAGCAAAACGATCAGATACAAATCCTCGCTCGGTGTGAAAA	63116
QY	1126	CACACAAAATCTTGATTCCTTAAAAATTCCTGTTGACAGGCAAGTGTGAAATCC	1185
Db	63115	CACACAAAATCTTGATTCCTTAAAAATTCCTGTTGACAGGCAAGTGTGAAATCC	63056
QY	1186	CGACCGTTTGAGGTTTCGATGTCGCCGATTTTGGTTCATCCGACAAATCTTGTGCGAA	1245
Db	63055	CGTGAGTTTGCCATTTTCTCTATGCCCGATTTTGGTTCATCCGACAAATCTTGTGCGAA	62996
QY	1246	GGCGGTGAAATTCCTTTGGTAAACAAAGAAACAAATCGATCTTGGCGACGCGAGGAAA	1305
Db	62995	GGCGGTGAAATTCCTTTGGTAAACAAAGAAACAAATCGATCTTGGCGAGTGTGAGAAA	62936
QY	1306	ATGACCGTTCGCTGCTTGTGTGGACTTTTGTGACTTATGTGAACTTCGACGCGATAAAAACC	1365
Db	62935	ACGACAATCCGAACCTGCTGCGATTTTCTTGACCTATGTGAAATTCGACGCGATGCAACC	62876
QY	1366	GAACGCCCGCGCTCCAAACGAAAGCGCAGGATGAAAGAGGGGGCGACGAAGGGGTGTAGGC	1425
Db	62875	GAACGTCGCCGCCCAACCGAAGCGCAGGACGAAGAGAGGGACGAAGAGATACAGGC	62816
QY	1426	GTTGATAACCGTAAAGAAAGCGAAGACGAATTCGGCGATGAAGAAGCACCGGACGACAA	1485
Db	62815	GTTGATAGCGTCGAAGAAGCGAAGACGAAATTCGACGATGAAGAAGGACCGCAAGACGCA	62756
QY	1486	GTCGTAGAGATGAAGACGAAGTGAACGACGAAGAAGAAATCGAAGAAGAACTCAAGAA	1545
Db	62755	GCCGTAAAGACGAAGGCGAGCGAAGAACGAAGCCGTA-----GAAGGT	62711
QY	1546	GAAGCTGAAGAGGAAAGAAACCCGAAGAAGAAATTCGCGCAGAAAGAGCAACCGCGTTCA	1605
Db	62710	GAAGATGAAGCTGAAGAACCCGAAGAAGAAATTCGCGCAGAAAGAGGCGGCGGTTCA	62651
QY	1606	GGCAGCATCTTGCCCATCTCCGAAGCGCTTAAAGCGAGGACATCGACTTTTCTGTAAA	1665
Db	62650	GACGCGATCTCTGCCGCTCCGGAAGCCCTTAAAGCGAGGAAATCGACTTTTCTGTAAA	62591
QY	1666	GGTATCCGACGCGCGAAGCCACATTCGCAAAAACGGAACGGCGATTTATACCGGCAC	1725
Db	62590	GGTATCCGACGCGCGAAGCCGATTTCCGAAAACTGGAGAGCACATATACCGGCAC	62531
QY	1726	TGGGAAGCGCGTATCGGCGTATCGGATAGTGGTAGCTTCATTCAAAGGATAGCTATGG	1785
Db	62530	TGGGAAGCGCGTATCGGC-----AAACCCATTCATATGGGCAATCATAGGCG	62486
QY	1786	---AATCAAGGGGCAAAACAGAAATTCAGTTGATTTTGAAGCGAGAGCGGTCCGGA	1842
Db	62485	GATAAAGAGCGCGCAAAAGCAGTATTTACCGTTGATTTCCGGAAGAAATCGATTTCCGGA	62425
QY	1843	ATGCTGACGAGAAAATGATCAACCCCGCTTTTATATTGAAAAAGGTGTGATTGAC	1902
Db	62425	ACGCTGACGAGGAAAACGGTGTGAACCTTGCTTTCCATATTGAAACGCAAGATTGAG	62366
QY	1903	GGTAACGGTTTCCACGCTTTGGCGCATATCTCGGAGAACCGGTATTGACCTTCTGGGCAG	1962
Db	62365	GGCAACGGTTTCTACGCGACAGCACGCACTTCGGGAGAACGCGCATCATCTTTCGGGAAT	62306
QY	1963	GGTTCGATTAACCGAAGAACTTCAAAGCCGAATCTTCTGTAAACAGCGGCTTTTAT	2022
Db	62305	GGTTTCGACGACCCCAAAACCTTCCAGCTAGTAATCTTCGTGTGAAGGGGATTTTAC	62246
QY	2023	GGCCCGAGCGCGCAGAAATTTGGCGGTAAATTTATTCGACAGCGACCGGAAATTCGGTGGC	2082
Db	62245	GGCCCGAGCGCGAGAAATTTGGCGGTATTTATTTCAATATGATGGGAAATCTCTTGGT	62186
QY	2083	GTATTTGGGCGCAAAAAGATGCAAGGAGG	2113

RESULT 6	AAAF21611/c
ID	AAF21611 standard; DNA; 34
XX	AAF21611;
XX	AAF21611;
XX	13-MAR-2001 (first entry)
DT	13-MAR-2001 (first entry)
XX	Neisseria meningitidis B n
DE	Neisseria meningitidis; Ne
KW	Neisseria meningitidis; detect
KW	diagnosis; antigen; detect
KW	ds.
XX	Neisseria meningitidis.
OS	Neisseria meningitidis.

XX PN WO200066791-A1.

XX
09-NOV-2000-

XX

PF 08-MAR-2000; 2000NOV03003320: XX

PR 30-APR-1999; 99US-0132068P.

PR 28-FEB-2000; 2000GB/00004695.

XX
 13 /CUTP \ CITRON CORP.

PA (GENO-) INST GENOMIC RES.

XX Pizza M, Hickey E, Peterson J, Tettelin H, Venter JC;
PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Frazer CM, Grandi G;

XX
DR WPI: 2000-647603/62.

XX Neisseria meningitidis B full length genome sequence and open reading
PT frames are used to detect treat and prevent Neisserial infections.

XX
pg
claim 7. Appendix A: 692pp: English:

XX
CC The present invention describes the full length genome of *Neisseria*
CC meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613
CC represent fragments of the NMB genomic sequence, as the sequence was too
CC long to go in a record on its own it was split into 8 sequences by 49980 bp
CC overlap each other at the beginning and end of each sequence by 49980 bp
CC (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of
CC AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of
CC AAF21608, and so on). AAF21545 to AAF21588 encode the *Neisseria* proteins
CC AAF21607, and so on). AAF21545 and AAF21589 to AAF21606 represent PCR
CC primers which are used in the exemplification of the present invention.
CC The NMB genome and fragments from it have antibacterial activity, and can
CC be used in vaccines and gene therapy. *Neisseria* nucleic acids, proteins
CC and/or antibodies which binds to the proteins can be used in compositions
CC for treating or preventing infection due to *Neisseria* bacteria or as a
CC diagnostic reagent for detecting the presence of *Neisseria* bacteria or
CC of antibodies raised to *Neisseria* bacteria. Computers, computer memory,
CC computer storage medium or computer databases can be used in a search to
CC identify open reading frames (ORFs) or coding sequences within the NMB
CC genome. The DNA sequences provide further opportunities to find antigenic
CC or immunogenic proteins which are more effective in vaccines than the
CC outer membrane proteins currently used

XX	03501	C	84627	G	84663	T	0	U	0	Other
XX	03501	C	84627	G	84663	T	0	U	0	Other

sequence 349980 BF, 07103 in, 000000

Query Match 64.8%; Score 13/5.4; DB 5; Length 515500
Best Local Similarity 80.2%; Pred. No. 0;

1 ATGTGTAACCGAATTATGGCGGCATTGTCTTGTGGCCCTTACTTTGGCATCTTGCAATC 60

XX AC AAX23319;
XX DT 11-JUN-1999 (first entry)
XX DE N. meningitidis strain BNCV LbpB cDNA.
XX KW LbpB; lactoferrin binding protein; vaccine; neisserial disease;
XX KW meningitis; diagnosis; treatment; ds.
XX OS Neisseria meningitidis.
XX FT Location/Qualifiers
XX FT 100..2277
XX FT /*tag= a
XX FT /product= "LbpB"
XX WO9909176-A1.
XX 25-FEB-1999.
XX 10-AUG-1998; 98WO-EP005117.
XX 15-AUG-1997; 97GB-00017423.
XX 05-FEB-1998; 98GB-00002544.
XX (UYUT-) RIJKSUNIV UTRECHT.
XX PA (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING NV.
XX XX Pettersson-Fernholm AM, Tommassen JPM;
XX PI WPI; 1999-190165/16.
XX DR P-PSDB; AAW93492.
XX DR New lactoferrin-binding protein B polynucleotides - obtained from
XX XX Neisseria meningitidis, used to develop products for the diagnosis,
XX PT prevention and treatment of neisserial disease, e.g. meningitis.
XX PT Claim 2; Page 74-78; 116pp; English.
XX PS This invention describes novel lactoferrin-binding protein B (LbpB)
XX CC strains of Neisseria meningitidis. The products of this invention can be
XX CC used for vaccinating humans against neisserial disease e.g. meningitis.
XX CC Antibodies raised against the proteins of the invention can be used for
XX CC diagnosing or treating neisserial disease in humans. The LbpB
XX CC polypeptides can also be used for identifying compounds which inhibit the
XX CC polypeptides
XX SQ Sequence 2277 BP; 700 A; 469 C; 573 G; 535 T; 0 U; 0 Other;
Query Match 61.0%; Score 1296.2; DB 2; Length 2277;
Best Local Similarity 79.0%; Pred. No. 5.7e-312;
Matches 1672; Conservative 0; Mismatches 373; Indels 72; Gaps 8;
QY 1 ATGTGTAACCGAATTATGCGCGCATGTCTGTGCGCTTACTTTGGCATCTTGATC 60
DB 100 ATGTGTAACCGAATTATGCGCGCATGTCTGTGCGCTTACTTTGGCATCTTGATC 159
QY 61 GCGCGCAATTTCGCGTGACGCTGTGTGCAATCAACGCGACCGCGTACCCCGTCACT 120
DB 160 GCGCGCAATTTCGCGTGACGCTGTGTGCAATCAACGCGACCGCGTACCCCGTCACT 219
QY 121 TTCAAGTCTAAGGACGTTCCCACTTCGCGCTCTGCGGGTCTTCGGTAGAACAACGCG 180
DB 220 TTCAAGTCTAAGGACGTTCCCACTTCGCGCTCTGCGGGTCTTCGGTAGAACAACGCG 279
QY 181 GTCACCGACCGCGTGTGTGCGCAATGCGGTGTGTGACGCGCAATATTGCAACTTCT 240
DB 280 GTCACCGCGCGCGTGTGTGCGCAATGCGGTGTGTGACGCGCAATATTGCAACTTCT 339
QY 241 GATAGAGATGCAATGATTTTCCAAATAGCAAAACAAGCAGAGAAAGAGCTGCTGTAAA 300
DB 340 CGTGAGATGGCAGGAATTCCAAATAGCAAAACAAGCAGAGAAAGAGCTGCTGTAAA 399

301 GAGCAAGATATCCTGTTTATATCGTTTCAAAAAAGATCAACGTGAGAGCTTAAAGAT 360
DB 400 GAAGGTGATGTTCTGTTTATATCGTTTCAAAAGGAATTAACCTTCAACACTTAAAGC 459
QY 361 AAAATTGCTCAACCAATCTTACGCAAGCATTTACACATCGGAAGAAAGAAATAAAAA 420
DB 460 GAAATTCATAAAGCTGATTCGGATGTAGAAATTAGGACATCAGAAAAGGAATAAAAA 519
QY 421 TATGATTATAAATTTAGATGAGGTTATGTATATATACTAAAGACGGAAGATGAAT 480
DB 520 TATGATTATAAATTTAGATGAGGTTATGTATA---TGTAAAGGGAAGATGAAT 576
QY 481 GAGTGGACTTCAAAATTACAAGCATCTACCAACCGTTTGTGTTATGACGTTTGTATAT 540
DB 577 AAGTGGACTTCAGATTACAGCAGTTTCCAAACCGCTTAGGTTATGACGTTTGTATAT 636
QY 541 TATTCCGGAGAACATCTCTTCCAAATCTTTACCGAGCGGGAACGTTGAAATATTCCGGC 600
DB 637 TATTCCGGAGAACATCTCTTCCAAATCTTTACCGAGTGGGGAACGTTGAAATATTCTGGT 696
QY 601 AACTGGCAATATATGACCGATGCCATACGTCTCATGCAACAGAAAAGCAGAGATCTTAGC 660
DB 697 AACTGGCAATATATGACCGATGCCAAGCTCATCGAGCAGTAAAGC---GTTGGCATT 753
QY 661 GAAGATTGGGTTATATCGTTTATACGGTCAAAATGTTCGAGCAACTTCTTATGCTGG 720
DB 754 GACAATTTGGGTTATACACATTTTATGTTAAGCATGTTGTTGCAACTTCTTATGCGGT 813
QY 721 ACTGCCGACGACCGGAGGAAACATCTCGCAATATACGTTTAAATTTTCACCAAAAA 840
DB 814 AAGGATGTGACGAAAGGGAAGAAACATCTGCTAAATATACGTTAGATTTTCGTAACAA 873
QY 781 ACTCTGAATGCAAGCTGATTTAAATCAGTATGTGCAAAAGAGAGATGATCTTAAAAA 840
DB 874 ACCCTGACGGCGAGCTGATTTAAACCAATATGTCAAACCCAGTGAGAAGC---AAAA 930
QY 841 CCACCTGACCATTTACGACATTTACTGCAAAATTTGGAAGCAACCGCTTTACCGCGAGTGC 900
DB 931 CGCTGACCATTTTCAACATCTACTCGCATTTTAAACGCGCAACCGCTTTACCGCGAGTGC 990
QY 901 AAGTTAACACAGAGTGNAGAGCATCAGCTGATATAAGATATTTGTTTTCATATAC 960
DB 991 AAGTCAATTCCTGATTTAGCGAAAGCCATGCAATAGAGCATTTGTTTTCATGTC 1050
QY 961 GATCGCATCAGCGCTTACGCGCGGTTTTCGCGGATAGGGGGAAGAGCTTTCGCGGA 1020
DB 1051 GATCGCATCAGCGCTTACGCGCGGTTTTCGCGGATAGGGGGAAGAGCTTTCGCGGA 1110
QY 1021 CGGTTTATCAGCAACGACCAACAGCTGATTCGGGCTGTTTCGAGGCAACCAAAAAACAGAG 1080
DB 1111 CGGTTTATCAGCAACGACCAACAGCTGATTCGGGCTGATTCGAGGCAACCAAAAAACAGAG 1168
QY 1081 ACAGCAACGACATCAGATCAAAATCTGCGCTCTGCGCTGGAACCAACCAAAAACTTG 1140
DB 1169 -----CGTGGCTCTGGAACCAACCAAAAACTTG 1200
QY 1141 GATTTCTAAAAATTTCCGTTGACGAGGCAAGTGTGAAATCCCGACCGCTTGAAGTT 1200
DB 1201 GATTTCTGAAATTTCCGTTGATGAGGCAAGTGTGAAATCCCGACCGCTTGAAGTT 1260
QY 1201 TCCATATGCGCGGATTTGTTGTCGACAAACTTCTTTCGAGGCGCTGAAATTCCT 1260
DB 1261 TCTCTATGCGCGATTTTGGTTCATCCGACAAACTTCTTTCGAGGCGCTGAAATTCCT 1320
QY 1261 TTGTTAAACAAAGAACCAACATCGATCTTTCGAGGCGGCAAGAAATGACCGCTCGTGT 1320
DB 1321 TTGTTAGCAAGAGAAACCATTCAGCTTTCGCGACGCGAGGAAATGACCGCTCAGTGT 1380
QY 1321 TGTGCGCACTTTTTCACCTATGTGAATCTCGACGAGTAAACACGGAAGCCCGCGCTC 1380
DB 1381 TGTGCGCACTTTTTCACCTATGTGAATCTCGACGAGTAAACACGGAAGCCCGCGCTC 1440

QY	1381	CAACCGAAGCGCCAGGATGAAGAGGGGGAGAGAGGGTCTAGCGCTTGATACGGTAAA	1440
Db	1441	AAACCGAAGGCGCA-----GGACGAAGAGGATTCGACACTTGATATGCGCA	1488
QY	1441	GAAACCGAAGACGAAATCGCGATGAAGAAGCACCGGAGACGAAGTCGTAGAAGATGA	1500
Db	1489	GAAACCGAAGACGAAATCGCGATGAAGAAGGACCGACCAAGATGCACCGCAGAGAT	1548
QY	1501	GACGAAGATGAAGACGAAGAGAAATCGAAGAGAACCTGAAGAAGAGCTGAAGAGGAA	1560
Db	1549	GAGGCACGAGAGACGAGGCCACGAAAACGAAGACGGCGAAGAACGACGAAGCTGAA	1608
QY	1561	GAAACCGAAGAGAAATTCGCGCAGAGAAGAAAGCAACGGCGTTACAGGACGATCTCTGCC	1620
Db	1609	GAACTGAAGAAGATCGTCGCG---AGAGGCACGGCAGTTCAAACGCCATCTCTGCC	1665
QY	1621	ACTCCGAGAGCCTTAAGAGCAGGACATCGACCTTTTCTGAAAGGTATCCGCACGGCG	1680
Db	1666	GTCCCGAAGCCTTAAGAGCAGGATATGACCTTTTCTGAAAGGTATCCGCACGCA	1725
QY	1681	GAAACCGACATTCCAAACCAACGGACGCGATATACGGGACCTTGGGAAGCGGTATC	1740
Db	1726	GAAACGATATTCGCGAAACTGGAGAGACGCTATACCGGACCTTGGGAAGCGGTATC	1785
QY	1741	GGCGTATCGGATAGTGTAAGTTCATTCAAAGGATAGTATGGG---AATCAGGGGCA	1797
Db	1786	GGC-----AAACCCATTCAATGGGACATCATGCGGATTAAGAGCGGCA	1830
QY	1798	AAAGCAGAAATTACCGTTGATTTGGAAGCGAAGACGGTGTCCGAATGCTCACAGAAAA	1857
Db	1831	AAAGCAGTATTACCGTTGATTTGGCAAGAAATCGATTCCGGAAACGCTGACGAGAAA	1890
QY	1858	AATGATACACCCCGCTTTTATATTGAAAAAGGTGATGACGTTACCGTTTCGAT	1917
Db	1891	AACGGTGTAGAACCTGCTTCCGTTATGAAAACGGCGTGAATGAGGCAACGGTTCCAT	1950
QY	1918	GCTTTGGCGGATCTCGGAGAACGGTATTGACCTTCTGGCAGGGTTCGACTAAACCG	1977
Db	1951	GGGACAGCGCGACTCGGGATGACGCATCGACCTTTCGGGACGGGTTGCACAAACCG	2010
QY	1978	AAGAACTTCAGAGCCGACATCTTCTGTGAACAGGCGGCTTTATGGCCCGCAGCGGCA	2037
Db	2011	CAGATCTTCAGAGCTAATGATCTTCTGTAGAAAGGAGGATTTACGGCCCGAAGGCGAG	2070
QY	2038	GAAATGGCGGTAAATATTACACACCGACCGGAAATTCGGTCGGTATTTGGGGGAAA	2097
Db	2071	GAAATGGCGGTATATTTTCAATATGATGGGAATCTCTTGGTATAACTGAAGGTACT	2130
QY	2098	AAAGATGACAGGAGGC	2114
Db	2131	GAAATAAAGTTGAAGC	2147

RESULT 8
AAX23322

ID AAX23322 standard; cDNA; 2262 BP.

XX AC AAX23322;

THE
XX
1770

11-JUN-1999 (first entry)

XX
DE
yy
N. meningitidis strain M990 LbpB cDNA.

XX
KW
LbnB: lactoferrin binding

KW lapp; lactoferrin binding protein; vac
KW meningitis; diagnosis; treatment; ds.
yy

OS *Neisseria meningitidis*.

XX	Key	Location/Qualifiers
FH		
FM		
XX		

FT	CDS	1. .2262
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FT
/*tag= a
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FT yy
/product= "LbpB"

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WO9909176-A1.
 25-FEB-1999.
 10-AUG-1998; 98WO-EP005117.
 15-AUG-1997; 97GB-00017423.
 05-FEB-1998; 98GB-00002544.
 (UUT-) RIJKSUNIV UTRECHT.
 (TECH-) TECHNOLOGY FOUND TECHNOLOGIESTICHTING ST.
 Pettersson-Fernholm AM, Tommassen JPM;
 WPI; 1999-190165/16.
 P-PSDB; AAW93495.
 New lactoferrin-binding protein B polynucleotides - obtained from
 Neisseria meningitidis, used to develop products for the diagnosis,
 prevention and treatment of neisserial disease, e.g. meningitis.
 Claim 2; Page 98-102; 116pp; English.
 This invention describes novel lactoferrin-binding protein B (LbpB)
 strains of Neisseria meningitidis. The products of this invention can be
 used for vaccinating humans against neisserial disease e.g. meningitis.
 Antibodies raised against the proteins of the invention can be used for
 diagnosing or treating neisserial disease in humans. The LbpB
 polypeptides can also be used for identifying compounds which inhibit the
 polypeptides
 Sequence 2262 BP; 698 A; 487 C; 590 G; 487 T; 0 U; 0 Other;
 Query Match 60.8%; Score 1291.8; DB 2; Length 2262;
 Best Local Similarity 78.1%; Pred. No. 7.1e-311;
 Matches 1676; Conservative 0; Mismatches 417; Indels 54; Gaps 8;

Query Match	60.8%	Score 1291.8	DB 2	Length 2262
Best Local Similarity	78.1%	Pred. No. 7.1e-311		
Matches 1676	Conservative	0	Mismatches 417	Indels 54
			Gaps	8
QY	1	ATGTGTAACCGAATATGCGGCAATGTCTTGTGTGCGCTTACCTTTTGGCATCTTGATC	60	
DB	1	ATGTGTAACCGAATATGCGGCAATGTCTTGTGTGCGCTTACCTTTTGGCATCTTGATC	60	
QY	61	GGCGGCAATTTGCGGCTGCGACCTGTGTGTCGAATCAACGCCGACCGCG	108	
DB	61	GGCGGCAATTTGCGGCTGCGACCTGTGTGTCGAATCAACGCCGACCGCGCAACTCTGTCTA	120	
QY	109	TACCCGCTCACTTTTCAAGTCTAAGGACGTTCCACATTCGCTCTCGCGGCTTTCGGTGA	168	
DB	121	GATTCMAATCTTCCAAATCCTGCGATAAGCCCTGCTCCAGCTCTCTCGGAGCCTTCGGTA	180	
QY	169	GAACACCAACCGCGGTCAACCGACCCGCGCTTGTGTGCGGCAATGCGGCTGTGTGAGACGGAAT	228	
DB	181	GAATCACGCGGTCAAGCGGCCCGCGCTGCGGTGCGGCAATGCGGCTGCGCAAGGGCGAAT	240	
QY	229	ATTGCAACTTCTGATGAAGATGGCAATGATTTTCCAAATAGCAAAACAAGCAGAAAGAAAG	288	
DB	241	ATCGCAACTTTTGATATAAATGTAATGAAATTCCAATAGTAAGCAGCAGAGGAGTAT	300	
QY	289	CTGTCTGTTTAAAGAGAGAGATATCCTGTTTTTATACGGTTTCCAAAAAGATCAACGTTCAAG	348	
DB	301	CTGCGGCTCAAAGAGAGAGATATCCTGTTTTTAGACGGTACGCCGAAAGAACAGGCTGAC	360	
QY	349	CAGCTTTAAAGATAAATTCGTCAACCAATCTTACGGCAAGCAATTAACACATCGGAAAAG	408	
DB	361	AACTTTAAAGAGAAATCAACGACGGCATCTTAATGCACCAATCTACACGTCGGATTTA	420	
QY	409	AAAAATATAAAATATGATTATATAATTTCTAGATGACGGTTATGTATATATCTATAAAGACGGA	468	
DB	421	AAAGATGATCGGTATCAATATATAAATATGTCGCGGCCGGATATGTTTATCTAGATATGGA	480	
QY	469	AAAGATGAAATTAGTGGACTTCAAATPACAAAGCAGTCTACCAACCGGTTGGTTATGAC	528	
DB	481	ACAGATGAAATCGAACAGAACTCAGGCGGTAAGCGGGTTACCCACCGGTTAGGTTATGAC	540	

1615 GGCAACGGCGTTTCAGGCAGCATCTGCTCTGCTCTAGAAAGCTCTAAAGGCGAGGACATC 1674
1651 GACCTTTTCCTGAAAGGTATCCGACCGGAGCGGACATTTCCAAAAAAGCGAAACGGGCG 1710
1675 GACCTTTTCCTGAAAGGTATCCGACCGGAGCGGACATTTCCGAAAGCGGACGGG 1734
1711 CATTATACCGGCACCTTGGGAAAGCGGTATCGCGGTATCGGATAGTGGTACGTCCTTCAA 1770
1735 CATTATACCGGCACCTTGGGAAAGCGGTATCGGC-----AAACCCATTCAA 1779
1771 AAGGATAGCTATCGGAAT---CAAGGGGCAAAAGCAGAAATTTACCGTTGATTTGGAAGCG 1827
1780 TGGGACAATCAGCGCGATGMAAAAGCGCAAAAGCAGAAATTTACCGTTGATTTGGAACAAG 1839
1828 AAGACGGTGTCCGGAATGCTGACAGAAATAATGATACAAACCCCGCTTTTATATATGAA 1887
1840 AATCGAATTTCCGAAAGCTGACGAGCAAAACGGGTAGAACCTGCTTTCCATATGAA 1899
1888 AAGGTGTGATTGACGTTAAACGGTTTCCACGGTTTGGCGCATATCTCGGAGAAACGGTATT 1947
1900 GACGCAAGATTGATGGCAACGGTTTCCACGGCAGCAGCGCATCTCGGAGAGCGGCATC 1959
1948 GACCTTTTCGGCAGGGTTCGACTAACCCGAGAACTTCAAGCCGACAACTTCTCTTGTA 2007
1960 AATCTTTGGGAAATGGTTTCGACCGACCGCAAAACATTCAGCTAGTAACTTCTGTTGA 2019
2008 ACAGCGCGCTTTATGCGCCGCGAGCGGAGAAATTCGGCGGTAATATTATCGACAGCGAC 2067
2020 GAAGGAGGATTTTACGCGCGGAGCGGGGGAATTCGGCGGTACTATTTCAATATGAT 2079
2068 CGGAATTCGGTCGGTATTTCGGGCGCAAAAAGATGACAAGGAGGC 2114
2080 GGGAAATCTCTTAGTATACTGAAATATTGAAAATGAAGCTGAAGC 2126

RESULT 9
AA81482/C
ID AA81482 standard; DNA; 14652 BP.
XX AA81482;
XX
XX
DT 04-DEC-2000 (first entry)
XX
DE N. meningitidis partial DNA sequence gnm_30 SEQ ID NO:30.
XX
XX Neisseria meningitidis; Neisseria gonorrhoeae; genome; immunogenic;
XX antigen; vaccine; diagnosis; infection; antibacterial; identification;
KW Meningococcus B; MenB; ds.
XX
XX Neisseria meningitidis.
XX
XX WO200022430-A2.
XX
XX
PD 20-APR-2000.
XX
XX 08-OCT-1999; 99WO-US023573.
XX
XX 09-OCT-1998; 98US-0103794P.
XX 30-APR-1999; 99US-0132068P.
XX
XX (CHIR) CHIRON CORP.
XX
XX Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
PI Rappuoli R, Pizza M;
XX
XX (CHIR) CHIRON CORP.
XX
XX WPI; 2000-318079/27.
XX
XX Isolated nucleotide sequences of Neisseria meningitidis which can be used
XX in the diagnosis and treatment of N. meningitidis infection and other
XX Neisserial infections, for example, N.gonorrhoea.
XX
XX

Neisserial infections, for example, N.gonorrhoea.

Claim 7; Page 582-586; 1760pp; English.

The present invention describes methods of obtaining immunogenic proteins from *Neisseria* genomic sequences. AA81453 to AA82414 represent specifically claimed *Neisseria meningitidis* genomic DNA sequences; AA81260 to AA81303 and AA825620 to AA825663 represent *Neisseria* DNA sequences and their corresponding proteins; AA81254 to AA81259 and AA81304 to AA81321 represent PCR primers used in the isolation of *Neisseria meningitidis* DNA sequences; and AA81122 to AA81452 represent *Neisseria meningitidis* MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodies against them, can be used in the manufacture of a composition. The composition can be used as a medicament (or in the manufacture of a medicament) for treating, preventing or diagnosing infection due to *Neisseria* bacteria. For example, some of the identified proteins could be components of vaccines against *Meningococcus B*; against all serotypes; and/or against all pathogenic *Neisseria*. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious *Meningococcus B* vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than other more variable regions

Sequence 14652 BP; 3745 A; 4117 C; 3436 G; 3354 T; 0 U; 0 Other;

PS	Query Match	44.1%;	Score 937.4;	DB 3;	Length 14652;
XX	Best Local Similarity	81.2%;	Pred. No. 2.3e-222;		
	Matches 1155;	Conservative	0;	Mismatches 226;	Indels 42; Gaps 4;
CC	703	GCAATCTTATGCTGGACGTCGCGACGACCGGAGGGAACATCTCTCCGAATATACG	762		
CC	14652	GCAATCTTATGCTGGACGTCGCGACGACCGGAGGGAACATCTCTCCGAATATACG	14593		
CC	763	GTTAAATTCGACCAAAACCTCAATGGGAGCTGATTAATAATCAGTATGTCGAAAG	822		
CC	14592	GTTGATTTGATACAAACCTCAATGGGAGCTGATTAATAATCAGTATGTCGAAAT	14533		
CC	823	A-----GAGATGATCTCTAAACCACTGACCATTTTACGACATTTACTGCAAAATG	873		
CC	14532	AAAGATTAATCAATGAGCCCAAAACCGCTGACATTTACGACATTTACGCAACATG	14473		
CC	874	GAGCGAACCGCTTTACCGGAGTGCCAAAGTTAAACACAGAGTGGAACGATCAAGCT	933		
CC	14472	GAGCGAACCGCTTTACCGGAGTGCCAAAGTTAAACACAGAGTGGAACGATCAAGCT	14413		
CC	934	GATAAAGAAATATTTGTTTTCATACCGATCCGATCCGATCCGATCCGATCCGATCCG	993		
CC	14412	GATAAAGAAATATTTGTTTTCATACCGATCCGATCCGATCCGATCCGATCCGATCCG	14353		
CC	994	GCGGATAAGGGGAAGAGCTTGCGGAGCTGTTTATCAGCAACGACACAGCGATTCGGC	1053		
CC	14352	GCGGATAAGGGGAAGAGCTTGCGGAGCTGTTTATCAGCAACGACACAGCGATTCGGC	14293		
CC	1054	GTGTTTCGAGGCAACAAACAAACAGACAGCAAAACGATCAGATCAAAATCTGCGCTG	1113		
CC	14292	GTATTCGAGGCAACAAACAAACAGACAGCAAAACGATCAGATCAAAATCTGCGCTG	14233		
CC	1114	CCGTCTGGAACACACACCAAAATCTTGGATCTCTAAATAATTTCCGTTGACGGCAAGT	1173		
CC	14232	TGCTCTGGAACACACACCAAAATCTTGGATCTCTAAATAATTTCCGTTGACGGCAAGT	14173		
CC	1174	GTTGAAAATCTCCGACCGCTTGAGGTTTCCACTATCCGATTTTCGTCATCCGCAAA	1233		
CC	14172	GATAAATAATCCCGTGAGTTTGCAATTTCTCTATCCCGATTTTGGTCAATCCCGCAAA	14113		
CC	1234	CTTCTTGTGAGGGGCTGAATCTCTTGGTAAACAAACAAACCAATCATCTTGGC	1293		
CC	14112	CTTCTTGTGAGGGGCTGAATCTCTTGGTAAACAAACAAACCAATCATCTTGGC	14053		

QY	1294	GACGGCAGGAAATGACCGTCCGTGCTTCTCGACTTTTGTGACCTATGTGAAACTCGGA	1353
Db	14052	GATGTTAGGAAACGCAATTCGAACCTGCTGCGATTTTCTGACCTATGTGAAACTCGGA	13993
QY	1354	CGGATAAAACCGCAACGCGCCCGCTCCAAACCGAGCGCCAGGATCAAGAGGGGGACGAA	1413
Db	13992	CGGATGCAACCGCAACGCGCCCGCTCCAAACCGAGCGCCAGGATCAAGAGGGGGACGAA	13933
QY	1414	GAGGGTGTAGGCGTTGATAACCGTTAAAGAACGAGAGCAATCGCGATCAAGAAACG	1473
Db	13932	GAGGATACAGGGGTTGATAGCGTCAAGAGGCGAAGCAATCGACGATCAAGAGGC	13873
QY	1474	ACCGGAGACGAGTCTGATAGATCAAGACGAGATGAAGACGAGAGCAAGCAATCGAAGNA	1533
Db	13872	ACCGAAGACGAGCGGTTAAAGACGAGAGCGAGAGAGAGCAAGAGCGGTA-----	13822
QY	1534	GAACCTGAAGAAAGCTGAAGAGGAGAAACCCGAGAGAAATTCGCGCAGAGAGGC	1593
Db	13821	-----GAAGGTGAAGATGAAGCTGAAGAACCCGAGAGAAATTCGCGCAGAGAGGC	13768
QY	1594	AACGCGGCTTCAGGACGATCTGCGCCACTCGGAGGCTCTAAAGGAGGAGCATCGAC	1653
Db	13767	GGCAGCGGTTGAGACGCGCATCTGCGCGCTCGGAGGCGCTTAAAGGAGGAGCATCGAC	13708
QY	1654	CTTTTCTGAAAGGTATCCGACGCGGAGCGGACATTCGCAAAACGAGCGCGCAT	1713
Db	13707	CTTTTCTGAAAGGTATCCGACGCGGAGGAAACGATATTCGAAACCTGGAGAGACAC	13648
QY	1714	TATACCGGCACTTCGGAGGCGGTATCGGCGTATCGGATGTGTGCTCATTTCAAAG	1773
Db	13647	TATACCGGCACTTCGGAGGCGGTATCGGCGTATCGGATGTGTGCTCATTTCAAAG	13603
QY	1774	GATAGCTATGCG---AATCAGGGGAAAAGCAGATTTACGTTGATTTGAAAGCGAAG	1830
Db	13602	GACATCAGGCGGATTAAGAAACGCGCAAGAGCATTTTACCGTTGATTTTCGCAAGAA	13543
QY	1831	ACGCTGTCCGGAATGCTGACAGAAAAAATGATACACCCCGCTTTTATATTGAAAAA	1890
Db	13542	TCGATTTCCGGAACGCTGACGAGGAAACGCGTGTAGAACCTGCTTTCCATTTGAAAC	13483
QY	1891	GGTGTGATGACGGTACCGTTTCCAGCTTTGCGCATACTCGGAGAGACGTTATTGAC	1950
Db	13482	GGCAAGATTGAGGCAACGCTTCTACGCGACACGACGCTCGGAGAGCGCATCAAT	13423
QY	1951	CTTTTCGGCAGGTTGCACTAACCCGAGAACTTCAAAGCGACAAATCTTTTGTAAACA	2010
Db	13422	CTTTTCGGGAAATGGTTGACCGCCGACCCCAACCTTCCAGCTAGTATCTTCGTGTAGAA	13363
QY	2011	GGCGGCTTTTATGGCCCGCAGCGCGAGAAATTCGGCGGTAAATATTCGACAGCGCGG	2070
Db	13362	GGGGATTTTACGCGCGCAGCGGAGGAAATTCGGCGGTATTTTTCATTAATGATGGG	13303
QY	2071	AAATTCGTCGCGTATTTGCGGCGAAAAAAGATGACAAAGGAGG	2113
Db	13302	AAATCTCTGGTATACTGAAGGTACTGAAAAATAAGTTGATG	13260

RESULT 10

AAF91389
ID AAF91389 standard; DNA; 1000 BP.

XX AAF91389;

XX AAF91389;
DT 04-MAY-2001 (first entry)

XX N. meningitidis (serogroup B) LbpA gene upstream sequence, SEQ ID:15.

XX Modified Gram-negative bacterium; outer membrane vesicle; bleb; vaccine;
XX genetically modified; protective antigen expression; LPS detoxification;
KW LPS; lipid A; homologous recombination vector; immunisation;
KW immunoprotective; non-toxic; paediatric; cyclic; circular; ds.

OS	Neisseria meningitidis.	
XX	WO200109350-A2.	
PN		
XX		
PD	08-FEB-2001.	
XX		
PF	31-JUL-2000; 2000WO-EF007424.	
XX		
PR	03-AUG-1999; 99GB-00018319.	
XX		
PA	(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.	
XX	Berthel FJ, Dalemans WLJ, Denoel P, Dequesne G, Feron C, Lobet Y;	
PI	Poolman J, Thiry G, Thonnard J, Voet P;	
XX		
DR	WPI; 2001-138654/14.	
XX		
PT	New isolated polynucleotide useful for outer membrane vesicle preparation	
PT	from Gram-negative bacterial strain for vaccination of microbial	
PT	infections.	
XX		
PS	Claim 46; Page 81; 128pp; English.	
XX		
CC	The invention relates to a genetically-engineered outer membrane vesicle	
CC	(bleb) preparation from a Gram-negative bacterium for use as a vaccine.	
CC	The blebs of the invention are improved with respect to their	
CC	immunogenicity and toxicity by the introduction of one or more genetic	
CC	changes to the chromosome of the bacterium from which the blebs are	
CC	derived. The changes made include the upregulation of protective antigen	
CC	expression, the downregulation of immunodominant non-protective antigen	
CC	expression, and genetic changes which result in detoxification of the	
CC	Lipid A moiety of lipopolysaccharide (LPS). The invention also	
CC	encompasses modified Gram-negative bacterial strains from which the bleb	
CC	preparations are made, a vector suitable for performing recombination	
CC	events (for the generation of the modified bacterial strains),	
CC	bacterially-derived nucleic acid sequences used in such a vector, and an	
CC	immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole	
CC	cell vaccine suitable for paediatric use. The bleb preparation is useful	
CC	in the manufacture of a medicament for immunising a human host against a	
CC	disease caused by infection of one or more of the following: Neisseria	
CC	meningitidis, Neisseria gonorrhoeae, Haemophilus influenzae, Moraxella	
CC	catarrhalis, Pseudomonas aeruginosa, Chlamydia trachomatis, and Chlamydia	
CC	pneumonia. The invention may also be used to provide immunisation against	
CC	the influenza virus. Bacterially derived nucleotide sequences of the	
CC	invention are used in the performance of homologous recombination events	
CC	up to 1000 bp upstream of a bacterial chromosomal gene in order to either	
CC	increase or decrease expression of that gene. Immunoprotective and non-	
CC	toxic Gram-negative bleb, ghost, or killed whole cell vaccines are more	
CC	immunogenic, less toxic and safer, and are particularly useful for	
CC	paediatric use. The present sequence represents a specifically claimed	
CC	Neisseria meningitidis nucleic acid sequence	
XX		
SQ	Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;	
	Query Match 23.4%; Score 497.6; DB 4; Length 1000;	
	Best Local Similarity 75.8%; Pred. No. 2e-113;	
	Matches 679; Conservative 0; Mismatches 189; Indels 28; Gaps 4;	
QY	1213 GATTTTGGTTCATCCCGACAACTCTTGTGCGAGGGCGTGAATTCCTTTGGTAAACAA 1272	
DB	1 GATTTTGGTTCATCCCGACAACTCTTGTGCGAGGGCGTGAATTCCTTTGGTAAACAA 60	
QY	1273 GAACAAACCATCGATCTTCGCGACGCGAGAAATGACCGTCCGTCCTTTGTCGACTTT 1332	
DB	61 GAGAAACCATCAAGCTTCGCGATGCGAGAAATGACCGTCCGTCCTTTGTCGACTTT 120	
QY	1333 TTGACCTTGTGAATTCGCGACGCGAGAAATGACCGTCCGTCCTTTGTCGACTTT 1392	
DB	121 TTGACCTTGTGAATTCGCGACGCGAGAAATGACCGTCCGTCCTTTGTCGACTTT 180	
QY	1393 CAGGATGAAGAGGGGACGAGAGGGGTGTAGCGCTTGATTAACGGTTAAGAAACGAGAC 1452	
DB	181 GAAGATAAAGGGAGGATGAAGAGGTGTCAGGGGTTGGTAAACGTCGAGAGGCGAAGGC 240	

QY	1453 GAAATCGCGCATGAAGAAGACACCGGAGACCGAAGTCGTAGAGATGAAGACGAGATGAA 1512	
DB	241 GAAATTCGCGAAGTGA-----AGCGAAGAAGCCGAGAAATCGTCGAAGAAGAA 291	
QY	1513 GACGAAGAAGAAATCGAAGAAGAACCTGAAAGAAGAGCTGAAGAGGAGAACCCGAGAA 1572	
DB	292 CCCGAAGAAGAGCTGAAGAAGAGAAAGCTGAAACCCCAAGAGAGTTGAAGAAACCGAAGAA 351	
QY	1573 GAAATTCGCGCAGAAAGGCAACGGCGGTTTCAGGAGAGCATCTTCGCCACTTCGGAAGACC 1632	
DB	352 AAATTCGCGCAGAAAGGCAACGGCGGTTTCAGGAGAGCATCTTCGCCACTTCGGAAGACC 411	
QY	1633 TCTAAAGGCGAGGACATCGACCTTTTCTGAAAGGTATCCGACGCGGCGGAAGCCGACATT 1692	
DB	412 TCTAAAGGCGAGGACATCGACCTTTTCTGAAAGGTATCCGACGCGGCGGAAGCCGACATT 471	
QY	1693 CCAAAAAACGGAACGGCGCATTTATACCGGCACCTTGGGAAGCGGTATCGGTCATCGAT 1752	
DB	472 CCAAGAACCGGAAGAACGACATATACCGGCACCTTGGGAAGCGGTATCGGTCATCGGTC 522	
QY	1753 AGTGGTACGTCCTTCAAAAAGGATAGCTATGCG-----AATCAAGGGGCAAAAGCAGAAATTT 1809	
DB	523 -----ACACCCATTCAATGGACATTCAGGCGGATTAAGAGCGGCAAAAGCAGAAATTT 576	
QY	1810 ACCGTTGATTTTCGAAGCGAAGACGGTGTCCGGAATGTGACAGAAAAAATGATACAAACC 1869	
DB	577 ACCGTTGATTTTCGAAGCGAAGATGATTTTCGGAACGCTGACGGAGAAAAACGGTGTACAA 636	
QY	1870 CCOCCTTTTATATGAAAAAGGTGTGATTCACGGTACGGTTTCCAGCGCTTTGGCGCAT 1929	
DB	637 CCGTCTTCTATTTGAAAAACGGCAAGATTGAGGCGCAACGGTTTCCAGCAACAGCAGCG 696	
QY	1930 ACTCGGAGACGGTATTGACCTTTTCGGCAGAGGTTTCGACTAACCCGGAAGAACTTCAAA 1989	
DB	697 ACTCGTGAAGACGGCATCAATCTTTCGGGAAATGGTTCGACCAACCCGAGAACCTTCCAA 756	
QY	1990 GCCGACAACTCTTCTTTGAACAGCGCGCTTTTATGCGCCGCGAGCGGCGAGATTGGCGGT 2049	
DB	757 GCTAGTGATCTTCGTGTAGAGGAGGATTTTACGCGCCGCGCA--GCGAGAGAAATTGGCGGT 815	
QY	2050 AATATTATCGACAGGACCGGAAATTCGTCGGTGTATTGGGGCGCAAAAAGATCA 2105	
DB	816 ATTATTTTCAATAGGATGGGAAATCTCTGTGTATACTGAAGGTACTGAAATAA 871	
	RESULT 11	
	ABK37769	
ID	ABK37769 standard; DNA; 1000 BP.	
AC	XX	
XX	ABK37769;	
DT	08-MAY-2002 (first entry)	
DE	DNA sequence upstream of LbpA #1 gene.	
KW	Upstream sequence; ds; Antibacterial; vaccine; bleb;	
KW	Gram-negative bacteria; outer membrane; LPS; lipopolysaccharide;	
KW	meningitis; bacteraemia; otitis media; pneumonia; chronic bronchitis;	
XX	sinusitis.	
OS	Neisseria meningitidis serogroup B.	
PN	WO200209746-A2.	
XX		
PD	07-FEB-2002.	
XX		
PF	31-JUL-2001; 2001WO-EF008857.	
XX		
PR	31-JUL-2000; 2000WO-EF007424.	
PR	08-FEB-2001; 2001GB-00003170.	
XX		
PA	(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.	

XX Berthet FJ, Dalemans W, Denoel P, Dequesne G, Feron C, Garcon N;
 PI Lobet Y, Poolman J, Thiry G, Thonnard J, Voet P;
 XX WP1; 2002-188688/24.
 DR
 XX
 PT New immunogenic composition comprising an antigen derived from a pathogen
 PT and a biep preparation from *Neisseria meningitidis*, useful as a vaccine
 PT for treating or preventing disease caused by the pathogen.
 XX
 XX Disclosure; Page 84; 125pp; English.
 PS
 XX The invention relates to an immunogenic composition comprising an antigen
 CC derived from a pathogen capable of protecting a host against the
 CC pathogen, mixed with an adjuvant comprising a biep preparation derived
 CC from a Gram-negative bacterial strain. The immunogenic composition
 CC consists of *N. meningitidis* B blebs or *N. meningitidis* C polysaccharide
 CC antigen. The blebs (derived from the outer membrane) may also have their
 CC toxic lipopolysaccharide (LPS) content reduced using heterologous down
 CC regulating sequences for LPS pathway genes or by up regulating genes
 CC involved in LPS synthesis suppression, by a promoter replacement
 CC technique. The immunogenic preparation is useful in the manufacture of a
 CC medicament for the treatment of a disease caused by the pathogen from
 CC which the antigen is derived (e.g. from *Neisseria meningitidis* and
 CC bacteraemia, from Moraxella, otitis media and pneumonia, and from H.
 CC influenzae chronic bronchitis, sinusitis, pneumonia and otitis media).
 CC The biep derived from *M. catarrhalis* or from a non-typeable *H. influenzae*
 CC is useful as an adjuvant in an immunogenic composition comprising one or
 CC more pneumococcal capsular polysaccharides or protein antigens. The
 CC present sequence is an upstream sequence from an *N. meningitidis*,
 CC *H. influenzae* or *M. catarrhalis* gene involved in LPS biosynthesis, which
 CC either up regulates or down regulates sequences to which it is attached
 CC
 XX Sequence 1000 BP; 328 A; 203 C; 278 G; 191 T; 0 U; 0 Other;
 SQ
 Query Match 23.4%; Score 497.6; DB 6; Length 1000;
 Best Local Similarity 75.8%; Pred. No. 2e-113;
 Matches 679; Conservative 0; Mismatches 189; Indels 28; Gaps 4;
 QY 1213 GATTTCGTATCCCGACAACTCTTCTGCGAGGGCGTGAATTCCTTGGTAAACAAA 1272
 DB 1 GATTTCGTATCCCGACAACTCTTCTGCGAGGGCGTGAATTCCTTGGTAAACAAA 60
 QY 1273 GAACAAACCATCGATCTTCCGCGAGGAGGAAATGACCGTCCGTCTGTCGACATTT 1332
 DB 61 GAGAAAACCATCAAGTTGCGATGCGAGGAATGACCGTCCGTCTGTCGACATTT 120
 QY 1333 TTGACCTATGTGAATCTCGACGGATAAACCGAACCGCCCGCTCCAAACCGAAGCG 1392
 DB 121 TTGACCTATGTGAATCTCGACGGATAAACCGAACCGCCCGCTCCAAACCGAAGCG 180
 QY 1393 CAGGATGAAGAGGGGACGAAGAGGTGTAGCGTTGATTAACCGTAAAGAACGGAAGAC 1452
 DB 181 GAAGATAAAGGAGGAGATGAAGAGAGTCGAGCGTGGTAAACGTCGAAGAGCGAAGGC 240
 QY 1453 GAAATCGGGATGAAGAAACACCGGAGAGCAAGTCTGAAGATGAAGACGAAGATGA 1512
 DB 241 GAAGTTCCGACATGA-----AGCGAAGAGCCGGAAGAAATCGTCGAAGAGAA 291
 QY 1513 GACGAGAGAGAAATCGAAGAGAACTCTGAAGAGAGCTGAAGAGGAACCCGGAAGAA 1572
 DB 292 CCGAAGAGAGAGCTGAAGAGGAAGAGCTGAACCCAAAGAGTCTGAAGAAACCGAAGAA 351
 QY 1573 GAATTCGCCGCAAGAAAGCAACGCGGTTCAGGCAGCATCTCGCCCATCTCGGAAGCC 1632
 DB 352 AATTCGCCGCAAGAAAGCAACGCGGTTCAGGCAGCATCTCGCCCATCTCGGAAGCC 411
 QY 1633 TCTAAGGAGGAGACATCGACCTTTTCTGAAAGGTATCCGACGCGGAAACCGACATTT 1692
 DB 412 TCTAAGGAGGAGACATCGACCTTTTCTGAAAGGTATCCGACGCGGAAACCGACATTT 471
 QY 1693 CCAGAAACCGAAGCGGCGCATTAATCCGCACTTGGAGAGCGCGTATCGGCGTATCGGAT 1752

Db 472 CCAGAACCGGAAAAAGCACATATACCGGCACCTTGGAGCGGTATCGGC----- 522
 QY 1753 AGTGGTAGCTCCATTCAAAAGAGTAGTATGCG---AATCAAGGGGCAAAAGCAGATTT 1809
 Db 523 -----ACACCCATTCAATGGGACATCAGCGCGGATAAAGAGCGGCAAAAGCAGATTT 576
 QY 1810 ACGTTGATTTCGAACGAGACGCGTGTCCGGAATCTGCAGAAAAAATGATACAAACC 1869
 Db 577 ACGTTTAAATTCGGCGAGAAATCGATTCCGGAACGCTCAGGAGAAAAACGGTGACAA 636
 QY 1870 CCGCTTTTATATTGAAAAAGGTGATTGACGGTAACGGTTTCCACGCTTTGGCGCAT 1929
 Db 637 CTTGCTTTCTATATTGAAAAACGCAAGATTGAGGCAACGGTTTCCACCAACAGACGC 696
 QY 1930 ACTCGGAGAACGGTATTGACCTTTCTTGGCAGGTTTCGACTAACCCGGAAGAACTTCAA 1989
 Db 697 ACTCGTGAAGCGGATCAATCTTTGGGAAATGGTTGACCAACCCGGAACCTTCCAA 756
 QY 1990 GCCGACAAATCTTCTTTGTAACAGCGCGCTTTTATGCGCGCGCAGCGCAGAAATGGCGGT 2049
 Db 757 GCTAGTGAATCTCGTGTAGAGGAGATTTTACGCCCGCGCA-GCGAGGAATTTGGCGGT 815
 QY 2050 AATATTATCGACAGCGACCGGAAATTCGGTTCGGTATTGGCGCGGAAAAAGATGA 2105
 Db 816 ATTATTTTCAATAGGATGGGAAATCTCTTGGTATACTGAAGGTACTCGAAATTA 871
 RESULT 12
 AAA81815
 ID AAA81815 standard; DNA; 707 BP.
 XX
 AC AAA81815;
 XX
 DT 04-DEC-2000 (first entry)
 DE N. meningitidis partial DNA sequence gnm_362 SEQ ID NO:362.
 XX
 KW *Neisseria meningitidis*; *Neisseria gonorrhoeae*; genome; immunogenic;
 KW antigen; vaccine; diagnosis; infection; antibacterial; identification;
 KW *Meningococcus B*; MenB; ds.
 XX
 OS *Neisseria meningitidis*.
 XX WO200022430-A2.
 PN
 XX 20-APR-2000.
 PD
 XX 08-OCT-1999; 99WO-US023573.
 PF
 XX 09-OCT-1998; 98US-0103794P.
 PR 30-APR-1999; 99US-0132068P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Frazer CM, Hickey E, Peterson J, Tettelin H, Venter JC;
 PI Masignani V, Galeotti C, Mora M, Ratti G, Scarselli M, Scarlato V;
 PI Rappuoli R, Pizza M;
 XX WPI; 2000-318079/27.
 DR
 XX Isolated nucleotide sequences of *Neisseria meningitidis* which can be used
 PT in the diagnosis and treatment of *N. meningitidis* infection and other
 PT *Neisseria* infections, for example, *N. gonorrhoea*.
 XX
 PS Claim 7; Page 1606; 1760pp; English.
 CC The present invention describes methods of obtaining immunogenic proteins
 CC from *Neisseria* genomic sequences. AAA81453 to AAA82414 represent
 CC specifically claimed *Neisseria meningitidis* genomic DNA sequences;
 CC AAA81260 to AAA81303 and AAB25620 to AAB25663 represent *Neisseria* DNA
 CC sequences and their corresponding proteins; AAA81254 to AAA81259 and
 CC AAA81304 to AAA81321 represent PCR primers used in the isolation of
 CC *Neisseria meningitidis* DNA sequences; and AAA81322 to AAA81452 represent

Query Match	20.2%;	Score 428.8;	DB 3;	Length 707;
Best Local Similarity	77.4%;	Pred. No. 2.3e-96;		
Matches	546;	Conservative 1;	Mismatches 149;	Indels 9; Gaps 2;
QY	23	GCAATTGCTCTGCTGCGCTTACTTTTGGCACTCTGCATCGCGGCGCAATTTGCGGTGCAAGC 82		
DB	1			
QY	83	CTGTGTGCGAATCAACGCGGACCGGTACCCCGTCACCTTCAAGTCTAAGAGAGCTTCCCA 142		
DB	61			
QY	143	CTTGGCTCTGCGCGGTCTTCGGTAGAAAAACACGCGGTCAACCGACCGCCGCTGGTG 202		
DB	121	CTCCGCCCTGCGCGGTCTTCGGTAGAAAAACACGCGGTCAACCGCGCCGCTGGTG 180		
QY	203	CGGCAATCGGCTGTTGAGACGGAATATTGCAACTTCTGATAAGGATGCGCAATGATTTTC 262		
DB	181			
QY	263	CAAAATAGCAAAACAAGCAGAAGAAAGCTGTGCTTTAAAGAGGAAGATATCCTGTTTTAT 322		
DB	241	CGGCAATCGGCTGCCAAGCGGAATATTGCTTCTATAACAAGACGTAACGGAATTC 240		
QY	323	ACGGTTCMAAAGAAAGATCAACGTACAGCAGCTTAAAGATAAAATTCGTCAACCAAAATCCCTA 382		
DB	301	ACGGTACGCTGAAGAAACAGCGCTGCAAACTTAAAGAAAGAAATCAACGACGGTATCTG 360		
QY	383	CGGCAAGCAATACCACTCGAAAAAGAAAAATAAAAAATATGATTATAAAATTTGATAGATG 442		
DB	361	ATGTGAGGTTATCATCTCAAAAAGAAAGAGAAAAATATCAATATCAATTTGTCGGTG 420		
QY	443	CAGGTTATGTATATATCTAAAGACGGAAG-----ATCAAAATGAGTGGACCTCAAATT 496		
DB	421	CGGGCTATGTTTACCGGGCGGAAGGAAGATAATGAAAAAGAAAAAGACTTCTGATG 480		
QY	497	ACAGCAAGTCTACCAACCGGTTGGTTATGACGGTTTCTATATTATTCGAGAGAACATC 556		
DB	481	GTAAGAGGTTTGTTAAACCGATTAGTATTGACGGTTTGTATATTATTCGAGAGAACATC 540		
QY	557	CTTTCGCAATCTTTTACCGAGCGCGGGAACCGGTGAAATATTCGCGCAACTGGCAATATATGA 616		
DB	541	CTTCCCAATCTTTACCGAGCGCGGGAACCGGTGCAATATTCGCGTAACTGGCAATATATGA 600		
QY	617	CCGATGCCATACGTCATCGAACAGSAAAAAGCAGGAGATCTACCGAAGATTTGGGTATA 676		
DB	601	CCGATGCCAAACGTCATCGCACANGTAAGGC---GGTTTTCAGTACGGATTTGGGTATA 657		
QY	677	TCGTTTATTACGCTCAAAATGTCGGAGCACTTCTTATGCTGCGA 721		
DB	658	CCACATATTGTTAAATGAAATGGGCAACTTCTTATGAGGCTA 702		

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 12:38:10 ; Search time 154.323 Seconds
(without alignments)
7637.968 Million cell updates/sec

Title: US-10-735-098-9
Perfect score: 2124
Sequence: 1 atgtgtaaacgcaattatgg.....acaaggaggaacacgatga 2124

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	86.2	4.1	7218	1	US-08-232-463-14
C 2	86	4.0	929	4	US-09-671-317-14
C 3	86	4.0	1001	4	US-09-671-317-14
C 4	79.8	3.8	43795	3	US-08-742-185-101
C 5	75.8	3.6	2223	1	US-08-257-073-4
C 6	74.8	3.5	3211	2	US-08-574-959A-8
C 7	74.8	3.5	3211	3	US-09-357-014-8
C 8	74.8	3.5	3901	2	US-08-574-959A-6
C 9	74.8	3.5	3901	3	US-09-357-014-6
C 10	74.4	3.5	16442	3	US-08-781-891-208
C 11	74.4	3.5	16442	4	US-09-618-166-208
C 12	71.4	3.4	390	3	US-09-197-649-7
C 13	69.4	3.3	1276	3	US-09-177-325-2
C 14	69.4	3.3	1276	3	US-09-411-812A-2
C 15	69.4	3.3	1276	3	US-09-590-113-2
C 16	69.2	3.3	3337	1	US-08-072-610-1
C 17	69.2	3.3	3337	2	US-08-719-822B-1
C 18	69.2	3.3	3337	3	US-09-092-458-1
C 19	68.4	3.2	966	4	US-08-766-738-2
C 20	68.4	3.2	966	4	US-09-262-610-2
C 21	67.2	3.2	1236	2	US-08-741-134-5
C 22	65.4	3.1	5394	3	US-08-688-376-1
C 23	65	3.1	3489	4	US-08-728-323A-1
C 24	65	3.1	3489	4	US-09-298-568-1
C 25	65	3.1	3489	4	US-09-410-399-1
C 26	65	3.1	32207	4	US-08-770-379-20
C 27	65	3.1	32207	3	US-08-757-669A-20

C	28	65	3.1	32207	4	US-09-230-371A-20	Sequence 20, Appl
	29	64.8	3.1	2230	3	US-08-448-194-7	Sequence 7, Appl
	30	64.8	3.1	2230	4	US-08-867-921-7	Sequence 7, Appl
	31	64.4	3.0	2106	3	US-08-613-009A-4	Sequence 4, Appl
	32	64.4	3.0	2106	4	US-08-613-009A-4	Sequence 4, Appl
	33	64.4	3.0	2106	4	US-08-778-570B-4	Sequence 4, Appl
	34	64.4	3.0	2106	4	US-09-059-584-4	Sequence 4, Appl
	35	64.4	3.0	2247	3	US-08-613-009A-3	Sequence 3, Appl
	36	64.4	3.0	2247	4	US-08-778-570B-3	Sequence 3, Appl
	37	64.4	3.0	8266	4	US-09-059-584-3	Sequence 3, Appl
	38	62.8	3.0	3955	4	US-09-059-584-54	Sequence 54, Appl
	39	61.6	2.9	1052	1	US-08-466-603-1	Sequence 207, Appl
	40	61.6	2.9	1052	1	US-08-314-503A-1	Sequence 1, Appl
	41	61.6	2.9	1052	1	US-08-468-066-1	Sequence 1, Appl
	42	61.6	2.9	1052	2	US-08-466-717-1	Sequence 1, Appl
	43	61.6	2.9	1052	3	US-08-466-743-1	Sequence 1, Appl
	44	61.6	2.9	1052	5	PCT-US95-12414-1	Sequence 1, Appl
	45	61.2	2.9	2139	4	US-09-059-584-50	Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
; Sequence 14, Application US/08232463;
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHREIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 28-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
; US-08-232-463-14

Query Match 4.1%; Score 86.2; DB 1; Length 7218;

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Best Local Similarity 4.0%; Pred. No. 2.7e-12;
Matches 16; Conservative 249; Mismatches 132; Indels 0; Gaps 0;

QY 1331 TTTTACCTATGAACTCGGACGATATAAACCGACCCCGCGTCCAAACCGAAG 1390
Db 1442 TTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1383
QY 1391 CGCAGGATGAAGGGGACGAGAGGTTGATAGCGTTGATAACGGTAAAGAAGGAAG 1450
Db 1382 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1323
QY 1451 ACGAATCGCGATGAAGAAGACCGGACGAGTGTAGAGATGAAGACGAATG 1510
Db 1322 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1263
QY 1511 AAGACGAAGAAGAAATCGAAGAGAACTTGAAGAAGAGTGAAGAGAAAGACCGGAAG 1570
Db 1262 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1203
QY 1571 AAGAAATTCGCGCAGAGAAGGCAACCGCGGTTGAGGAGATCTGCCCACTCCGGAAG 1630
Db 1202 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1143
QY 1631 CCTCTAAGCAGGACGATCGACCTTTCTGAAAGGTATCCGACGCGGAGCGGACCA 1690
Db 1142 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1083
QY 1691 TTCAAAAACGACGCGCATATATACCGGCCTG 1727
Db 1082 RRRRRRRRRRRRRRRATCGCAAGCTCCTCGACCTG 1046

RESULT 2
US-09-671-317-14/c
; Sequence 14, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 14
; LENGTH: 929
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-363 : polymorphic base A or G
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-363.mis1, potential
; NAME/KEY: misc_binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-454-363.mis2, potential complement
; NAME/KEY: primer_bind
; LOCATION: 139..158
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
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LOCATION: 634..652
OTHER INFORMATION: downstream amplification primer, complement
NAME/KEY: misc_binding
LOCATION: 489..513
OTHER INFORMATION: 12-454-363 potential probe
NAME/KEY: misc_feature
LOCATION: 674..679,881..882,892..893
OTHER INFORMATION: n=a, g, c or t
US-09-671-317-14

Query Match 4.0%; Score 86; DB 4; Length 929;
Best Local Similarity 64.4%; Pred. No. 1.1e-12;
Matches 139; Conservative 0; Mismatches 76; Indels 1; Gaps 1;

QY 1380 CCAACCGAGCGCGATGAAGAGGGGACGAGAGGGGTGTAGGGCTTGTATAACGGTAA 1439
Db 880 CCATCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 821
QY 1440 AGAAGCGAAGACGAATCGCGGATGAAGAAAGCAGCGGAGACGAGTCTAGAGATGA 1499
Db 820 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 761
QY 1500 AGACGAGATGAAGACCAAGAA-GAATATCGAAGAGAGACCTGAAAGAGAGAGCTGAAGAGG 1558
Db 760 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 701
QY 1559 AAGAACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1594
Db 700 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 665

RESULT 3
US-09-671-317-439/c
; Sequence 439, Application US/09671317
; Patent No. 6528260
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
; FILE REFERENCE: 62.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/671,317
; CURRENT FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 09/536,178
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT/IB00/00403
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,269
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 60/131,961
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 977
; SOFTWARE: Patent.pm
; SEQ ID NO 439
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-454-242 : deletion AT
; NAME/KEY: misc_binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-454-242.mis1, potential
; NAME/KEY: primer_bind
; LOCATION: 260..279
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer_bind
; LOCATION: 755..773
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc_feature
; LOCATION: 795..800
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OTHER INFORMATION: n=a, g, c or t
US-09-671-317-439

Query Match 4.0%; Score 86; DB 4; Length 1001;
Best Local Similarity 64.4%; Pred. No. 1.2e-12;
Matches 139; Conservative 0; Mismatches 76; Indels 1; Gaps 1;
QY 1380 CCAACCGAAGCGCAGGATGAAGAGGGGGACGAGGGGTGTAGGCGTTGATACGGTAA 1439
Db 1001 CCATCTCAAGAAGAAG 942
QY 1440 AGAAGCGAAGAGAAATCGCGGATGAAGAAACGACCGGAGACGAACTCGTAGAAGATGA 1499
Db 941 AGAAG 882
QY 1500 AGACGAGAGATGAAGACGAGAA-GAAATCGAAGAGAACTGAAGAGAAAGCTGAAGAGG 1558
Db 881 AGAAG 822
QY 1559 AAGAACCAGAGAGAGAAATTCGGCGCAGAGAGAGGCA 1594
Db 821 AAGAAG 786

RESULT 4

US-08-742-185-101
; Sequence 101, Application US/08742185
; Patent No. 6020476
; GENERAL INFORMATION:
; APPLICANT: Page, David C.
; APPLICANT: Reijo, Renee
; APPLICANT: Saxena, Richa
; APPLICANT: Hawkins, Trevor
; APPLICANT: Reeve, Mary Pat
; TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,185
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/690,734
; FILING DATE: 31-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/310,429
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH194-07A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43795 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-742-185-101

Query Match 3.8%; Score 79.8; DB 3; Length 43795;
Best Local Similarity 64.2%; Pred. No. 3e-10;
Matches 120; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 1388 AGCGCAGGATGAAGAGGGGGACGAGGGGTGTAGGCGTTGATACGGTAAAGAAACG 1447
Db 38855 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 38914
QY 1448 AAGACCAATCGCGGATGAAGAAAGCAGCCGAGACGAAAGTCCTAGAGATGAAGACGAAG 1507
Db 38915 AAGAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 38974
QY 1508 ATGAAGACCAAGAGAAATCGAAGAGAAACCTGAAGAGAAAGCTGAAGAGAAAGACCCG 1567
Db 38975 AAGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 39034
QY 1568 AAGAAGA 1574
Db 39035 AAGAAGA 39041

RESULT 5

US-08-257-073-4
; Sequence 4, Application US/08257073
; Patent No. 5766597
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: de Taisne, Charles
; APPLICANT: Tine, John A.
; TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,073
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,783
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,305
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,183
; FILING DATE: 20-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2570
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066 CURTMS
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2223 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-257-073-4

Query Match 3.6%; Score 75.8; DB 1; Length 2223;
Best Local Similarity 58.0%; Pred. No. 7.7e-10;
Matches 134; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 1454 AAATCGCGATGAAGAAAGCACCAGAGACGAAATCGTAGAAGATGAAGACGAAGATGAAG 1513
DB 2483 AGAAGACCTTTGAGGAAGAGAGATGAAGAGGAATATTTTGAAGAGGAAGAGAGG 2542
QY 1514 ACAGAGAGAAATCGAAGAAAGAACCTTGAAGAAAGCTGAAGAGGAAGAACCCGAGAG 1573
DB 2543 AGAAGAGAGAGTTTGAAGAAAGAAATTTGAGGAAGAGAGGTTAGTTAGGAAGAGAG 2602
QY 1574 AATTCGCGCAGAGAGAG 1591
DB 2603 AAGAGGAGGATGAGAGG 2620

QY 1357 ATAAAACGACGCCCGCGTCCACCAAGCGCAGGATGAAGAGGGGAGAGAG 1416
DB 1984 ATAGAAGCTGAAGTGGATGCCCTCGCACCAAAATTAAGGAAGAGAGAAAGAAA 2043
QY 1417 GGTGTAGCGTTGATACGGTAAAGAAAGCAAGACGAAATCGCGGATGAAGAAAGCACC 1476
DB 2044 GAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2103
QY 1477 GGACAGCAAGTCTGTAAGATGAAGACGAGATGAAGACGAGAAAGAAATCGAAGAGAA 1536
DB 2104 AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2163
QY 1537 CCTGAAGAGAGCTGAAGAGAGAGAACCCGAGAGAAATTCGCGGAGAA 1587
DB 2164 CAAGAAGAGAGAGAGAGAAATAGTACCGAGAAATTTGACACAGTGAAGAA 2214

RESULT 7
US-09-357-014-8
; Sequence 8, Application US/09357014
; Patent No. 6291645
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Joong, Ratna K. Vadlamudi
; and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/357,014
; FILING DATE: 19-Jul-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/574,959
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3211 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 439..3157
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-357-014-8

Query Match 3.5%; Score 74.8; DB 2; Length 3211;
Best Local Similarity 61.1%; Pred. No. 1.7e-09;
Matches 121; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1394 AGATGAAGAGCGGAGAGAGGTTGATACCGTTGATACCGTTGATACCGTTGATACCG 1453
DB 2423 AGGAAG 2482
QY 1454 AAATCGCGATGAAGAAAGCACCAGAGACGAAATCGTAGAAGATGAAGACGAAGATGAAG 1513
DB 2483 AGGAAGACTTTGAGGAAG 2542

US-08-574-959A-8
; Sequence 8, Application US/08574959A
; Patent No. 5962224
; GENERAL INFORMATION:
; APPLICANT: Jaekyoon Shin, Insil Joong, Ratna K. Vadlamudi
; APPLICANT: and Jack L. Strominger
; TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
; AND USES THEREFOR
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/574,959A
; FILING DATE: 19-DEC-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: DFN-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3211 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 439..3157
US-08-574-959A-8

Query Match 3.5%; Score 74.8; DB 2; Length 3211;
Best Local Similarity 61.1%; Pred. No. 1.7e-09;
Matches 121; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 1394 AGATGAAGAGCGGAGAGAGGTTGATACCGTTGATACCGTTGATACCGTTGATACCG 1453
DB 2423 AGGAAG 2482

Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-208
Query Match 3.5%; Score 74.4; DB 3; Length 16442;
Best Local Similarity 65.1%; Pred. No. 4.7e-09; Indels 1; Gaps 1;
Matches 125; Conservative 0; Mismatches 66;
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Db 16298 GGAGGAGCAGGAGGAGGAGCAGGA-GCAGGAGGAGGAGGAGGAGGAGGAGGAGG 16240
QY 1446 CGAAGACGAAATCGCGCATGAAGAAAGCCCGAGACGAGTCTGTAGAGATGAAGACGA 1505
Db 16239 AGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 16180
QY 1506 AGATGAAGACGAAAGAAATCGAAGAAACCTGAAGAAAGCTGAAGAGGAGGAGGAGGAG 1565
Db 16179 AGAAG 16120
QY 1566 CGAAGAGAAATT 1577
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RESULT 12
US-09-197-649-7
Sequence 7, Application US/09197649
Patent No. 6194550
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Tuerk, Craig
APPLICANT: Priebnow, David
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEX02/CI-CON
CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1998-11-23
EARLIER FILING DATE: 1992-01-31
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1991-08-01
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER FILING DATE: 1991-08-01
EARLIER APPLICATION NUMBER: 07/561,968

Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-208
Query Match 3.5%; Score 74.4; DB 3; Length 16442;
Best Local Similarity 65.1%; Pred. No. 4.7e-09; Indels 1; Gaps 1;
Matches 125; Conservative 0; Mismatches 66;
QY 1386 GAAGCGCAGGATGAAGAGGGGACGAAGAGGGTGTAGCGTGTATACCGTTAAAGAAAG 1445
Db 16298 GGAGGAGCAGGAGGAGGAGCAGGA-GCAGGAGGAGGAGGAGGAGGAGGAGGAGG 16240
QY 1446 CGAAGACGAAATCGCGCATGAAGAAAGCCCGAGACGAGTCTGTAGAGATGAAGACGA 1505
Db 16239 AGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 16180
QY 1506 AGATGAAGACGAAAGAAATCGAAGAAACCTGAAGAAAGCTGAAGAGGAGGAGGAGGAG 1565
Db 16179 AGAAG 16120
QY 1566 CGAAGAGAAATT 1577
Db 16119 AGAAGAGAAAT 16108
RESULT 11
US-09-618-166-208/c
Sequence 208, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO WERNER'S SYNDROME

Thu Aug 26 10:18:20 2004

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Query Match      3.3%; Score 69.4; DB 4; Length 1276;
Best Local Similarity 56.3%; Pred. No. 2.7e-08;
Matches 130; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

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QY 1419 TGTAAGCGTTGATTAACGTTAAAGAAAGCCAGACGAAATCGCGCATGAAGAAACCGG 1478
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1479 AGACCAAGTCTGTAGAGATGAAGACGAGATGAAGACGAGAGAAATCGAAGAGACC 1538
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QY 1539 TGAAGAGAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1589
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Search completed: August 25, 2004, 05:32:08
 Job time : 155.323 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 23:48:06 ; Search time 1069.14 Seconds
(without alignments)
9777.159 Million cell updates/sec

Title: US-10-735-098-9

Perfect score: 2124

Sequence: 1 atgtgttaaacggaattatgg.....acaaggaggcaacacgatga 2124

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 6474540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1499.8	70.6	2226	17	US-10-735-098-5
5	1296.2	61.0	2277	17	US-10-735-098-1
6	1291.8	60.8	2262	17	US-10-735-098-7
7	497.6	23.4	1000	17	US-10-343-561-15
8	104.6	4.9	3300	17	US-10-467-534-80
9	98.4	4.6	374849	13	US-10-087-192-1627
10	97.2	4.6	31124	13	US-10-087-192-463
11	96.6	4.5	37265	13	US-10-087-192-49
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c 16	93.8	4.4	496	9	US-09-864-761-2534	Sequence 2534, Ap
c 17	93.6	4.4	96602	16	US-10-085-117-61	Sequence 61, Appl
c 18	90.6	4.3	39443	16	US-10-085-117-313	Sequence 313, App
c 19	90.2	4.2	276	9	US-09-864-761-20595	Sequence 20595, A
c 20	89.6	4.2	32069	15	US-10-004-113-7	Sequence 7, Appli
c 21	89	4.2	48652	13	US-10-087-192-859	Sequence 859, App
c 22	88.6	4.2	96596	12	US-10-052-482-70	Sequence 70, Appl
c 23	88.6	4.2	96597	12	US-10-052-482-103	Sequence 103, App
c 24	88.4	4.2	522	14	US-10-101-487-71	Sequence 71, Appl
c 25	88.4	4.2	530	14	US-10-101-487-73	Sequence 73, Appl
c 26	88.4	4.2	554	14	US-10-101-487-69	Sequence 69, Appl
c 27	88.4	4.2	554	14	US-10-101-487-106	Sequence 106, App
c 28	88	4.1	54786	12	US-10-052-482-211	Sequence 211, App
c 29	87.2	4.1	225883	15	US-10-175-523-57	Sequence 57, Appl
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c 31	86	4.0	929	13	US-10-294-934-14	Sequence 14, Appl
c 32	86	4.0	1001	13	US-10-294-934-439	Sequence 439, App
c 33	86	4.0	143899	10	US-09-972-546-15	Sequence 15, Appl
c 34	85.6	4.0	4316	9	US-09-880-107-3713	Sequence 3713, Ap
c 35	85.6	4.0	4316	13	US-10-257-021-81	Sequence 81, Appl
c 36	85	4.0	559	9	US-09-864-761-7684	Sequence 7684, Ap
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c 39	84	4.0	286	15	US-10-029-386-18943	Sequence 18943, A
c 40	84	4.0	577	15	US-10-029-386-5187	Sequence 5187, Ap
c 41	84	4.0	138115	17	US-10-322-281-377	Sequence 377, App
c 42	83.6	3.9	536	15	US-10-029-386-19974	Sequence 19974, A
c 43	83.6	3.9	599	15	US-10-029-386-6243	Sequence 6243, Ap
c 44	83.6	3.9	33454	13	US-10-087-192-1111	Sequence 1111, Ap
c 45	83.2	3.9	6944	15	US-10-172-086-111	Sequence 111, App

ALIGNMENTS

RESULT 1

US-10-735-098-9
Sequence 9, Application US/10735098
Publication No. US20040131634A1
GENERAL INFORMATION:
APPLICANT: Pettersson-Fernholm, Annika Margareta
APPLICANT: Tomassen, Johannes Petrus Maria
TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
FILE REFERENCE: B45106C1
CURRENT APPLICATION NUMBER: US/10/735,098
CURRENT FILING DATE: 2003-12-12
PRIOR APPLICATION NUMBER: 09/485,760
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: PCT/EP98/05117
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: GB 9717423.9
PRIOR FILING DATE: 1997-08-15
PRIOR APPLICATION NUMBER: GB 9805544.8
PRIOR FILING DATE: 1998-02-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 2124
TYPE: DNA
ORGANISM: Neisseria meningitidis strain 881607
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2121)
US-10-735-098-9

Query Match 100.0%; Score 2124; DB 17; Length 2124;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 61 GGGGGCAATTTTCGGCGTCGACGCTGTTTGTGGAATCAACGCGGACCGCGTACCCCGTCACT 120
 QY 121 TTCAGTCTAAGAGAGTTCACACTTCGCTCTCGCGGTCCTCGGTAGAAACACGCGG 180
 Db 121 TTCAGTCTAAGAGAGTTCACACTTCGCTCTCGCGGTCCTCGGTAGAAACACGCGG 180
 QY 181 GTCACGACCGCGGTCGCGCAATGCGGCTGTTGAGACGGAATATTGCAACTTCT 240
 Db 181 GTCACGACCGCGGTCGCGCAATGCGGCTGTTGAGACGGAATATTGCAACTTCT 240
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 Db 361 AAAATTCGTCAACCAATCCTACGGCAAGCAATTAACCATCGGAAAGGAAATAAAAA 420
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; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tommassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735,098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485,760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2169
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain M981
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (2166)
US-10-735-098-3

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Best Local Similarity 84.5%; Pred. No. 0;

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Db	361	GAATTCATATAACGTAATCTCTGAGGCAAGCATATCCACATCGGAAAGAAAAATAAAAA	420
QY	421	TATGATTTATAAATTTGTPAGATGCAAGTATGTATATATACTAAAGACGCAAAAGATGAAT	480
Db	421	TATAAATTATCGGTTTGTGTCAGTGCCTGCGGTTATGTGTTTACTAAAACGGAAGAAGATGAAT	480
QY	481	GAGTGGACTTCAAAATTACAGAGATGTACCAACCGGTTTGGTTATGACGGTTTGTATAT	540
Db	481	GAGAAACAATCGGATGAAAGACAGTTTCTTAATCGTTTACGGCTATGACGGTTTGTATAT	540
QY	541	TATTCGCGAACAATCCTTCGCAATCTTTACGAGCGCGGGAACGGTGAATATTCCGGC	600
Db	541	TATCTCGGAGAACATCCTTCGCAATCTTTACGAGCGCGGGAACGGTGAATATTCCGGC	600
QY	601	AATGGCAATATATGACCGATGCCATACGTCATCGAACAGGAACGAGAGATCTTACG	660
Db	601	AATGGCAATATATGACCGATGCCATACGTCATCGGAAGAGTTAA---GGGGGTTCCAGT	657

QY	661	GAAGATTGGGTTATATCGTTTATTACGGTCAAAAATGTCGGAGCAACTCTTATGCTGCG	720
Db			
Db	658	GTGGAATTGGGTTATACCAATATATGGTAAATGGGCACGCTTCTTATGAGGCT	717
QY	721	ACTGCCAGCACCGGAGGGAACAATCTCGCGGAATATACGTTAAATTCGACCAAAAA	780
Db			
Db	718	AGGATGCGCATGCCCGGAAAAACATCTCTCGGAATAACGTTAAATTCGCACAAAAA	777
QY	781	ACTCTGAATGGCAAGCTGATTAAAAATCAGTATGTCAAAGAGAGATGATCCTAAAAAA	840
Db			
Db	778	AACCTGGAGGTAAAGTTGAATTAATAATCAGTATGTCAAAGAGAGATGATCCTAAAAAT	837
QY	841	CGTCTGACCAATTTACGACATTATGCAAAATTTGGACGGCAACCGCTTTTACGGCAGTCC	900
Db			
Db	838	CCACTGACCATTTACAAACATTACCGCAACATTTGACGGCAACCGCTTTTACGGCAGTCC	897
QY	901	AAAGTTAAACACAGAGGTGAAGACGAATACGCTGATAAAGAATATTTGTTTTTCCATACC	960
Db			
Db	898	AAAGTTAGCACCGAGGTGAAGACGAACACGCTGATAAAGAATATTTGTTTTTCCATACC	957
QY	961	GATGCCGATCAGCGGCTTGAGGCGCGTGTGCGCGATAGGCGGAAGACGTTGCCGGA	1020
Db			
Db	958	GATGCCGATCAGCGCTTGAGGCGCGTGTGCGCGATAGGCGGAAGACGTTGCCGCG	1017
QY	1021	CGGTTTATCAGCAACGACACAGCGTATTCGCGCGTGTTCGCAGGCAAAACAAAAACAGAG	1080
Db			
Db	1018	CGGTTTATCAGTAAACGACACAGCGTATTCGCGCGTGTTCGCAGGCAAAACAAAAACAGAG	1077
QY	1081	ACAGCAAAACGATCAGATACAAATCTGCGCTGCGGTCTGGAAACACACCAAAATCTTG	1140
Db			
Db	1078	ACAGCAAAACGATCAGATACAAATCTGCGCTGCGGTCTGGAAACACACCAAAATCTTG	1137
QY	1141	GATTCCTCTAAAAATTTTCGTTGACGAGCAAGTGTGAAATCCCGACCGTTTGAGTT	1200
Db			
Db	1138	GATTCCTCTAAAAATTTTCGTTGACGAGCGACTGATGACCATGCGCCGTAAGTTTGCCATT	1197
QY	1201	TCCACTATGCCCGATTTTGGTTCATCCGACAAAATCTTCGTGCAAGGGCGTGAAATTCCT	1260
Db			
Db	1198	TCCACTATGCCCGATTTTGGTTCATCCGACAAAATCTTCGTGCAAGGGCGTGAAATTCCT	1257
QY	1261	TTGTTAAACAAAGAACAAACCATCGATCTTGCAGACGCGAGGAAAATGACCGTCCGTGCT	1320
Db			
Db	1258	TTGTTAGCCAAAGAGAAAACCATCGACTTTCGCGACGGCAGGAAAATGACCATCCGTGCT	1317
QY	1321	TGTTGCGACTTTTGACTATGTGAACACTCGACCGGATAAAAACCGAAACGCGCCGCGTC	1380
Db			
Db	1318	TGTTGCGACTTTTGACTATGTGAACACTCGACCGGATAAAAACCGACCGCCGCGCGTC	1377
QY	1381	CAACCGAAGGCGAGGATGAAGAGGGGGACGAAGAGGGTGTAGGCGCTGATAACGATAA	1440
Db			
Db	1378	AAACCGAAGGCGAGGATGAAGAGGATTCGGAATTTGATGTAATGCGGAAGAAAGCAAGAC	1437
QY	1441	GAAGAA--GCCAAGACGGAATCGCGATGAGAAAGCACCCGGAGA	1481
Db			
Db	1438	GAATTTCCGAAGATGATAACCGCGAAGATGAAGTCAACGAAGAAGAGGAAGCTCAAGAA	1497
QY	1482	--CGAAGTCGTAGAAGTGAAGACGAAGATGAAGACGAAGAGAATCGAA-----GAA	1533
Db			
Db	1498	ACCGAAGAGAAACTGATGAACGACGAGAGGAGAACCGGAAGAATCTGAAGAAACTGAA	1557
QY	1534	GAACCTGAAGAGAGCTGAAGAGGAGAACCCGGAAGAAGATTTCCCGGCAGAGAAGGC	1593
Db			
Db	1558	GAAGCTGAAGAACTGAAGAAACTGAAGAAAATGAAAGAAAATCGCCGACGAGAGAAGGC	1617
QY	1594	AACGGCGGTTACGGCAGCATCTGCGCCACTCGGGAAGCCTTAAAGGACGGGACATCGAC	1653
Db			
Db	1618	AACGGCGGTTACGGCAGCATCTGCGCCACTCGGGAAGCCTTAAAGGACGGGACATCGAC	1677
QY	1654	CTTTTCTGAAAGGTTATCGCACGCGGAAGCCGACATTTCCAAAAACGGAACCGCGCAT	1713
Db			
Db	1678	CTTTTCTGAAAGGTTATCGCACGCGGAAGCCGACATTTCCGCAATTTGHAAGACGACGC	1737

Db	361	AAGGATAAAATTCATCAACCAATCTTAATGTAGAAATTTAGGACATCAGAAAATGAAAT	420
Qy	415	AAAAAATATCATATAAATTTAGATGCGAGGTTATCTATATATACTAAAGACGGAAGAAT	474
Db	421	AAAAAATATGTTAGAAATTTGTGATGCGGTTATGTATATATACTAAACCGGAACAGAT	480
Qy	475	GAAATTCAGTGGACTTCAAAATTAACAGAGTCTACCAACCGGTTTGGTTATGACGGTTT	534
Db	481	GAAATTCAGTGGACTTCAAAATTCGCAAGCAGTTTCTAAATCTGTTTGGCTACGACGGTTT	540
Qy	535	GTAATTTATTCGGAGAAACATCTTTCGCAATCTTTACCGGCGGGAACGGTGAATAT	594
Db	541	GTATATTTATTCGGAGAACATCTTTCGCAATCTTTACCGGCGGGAACGGTGAATAT	600
Qy	595	TCCGCAACTGCGCAATATATACCGATGCCATACGTCTCAACAGGAAAGACGAGGAT	654
Db	601	TCCGCAACTGCGCAATATATACCGATGCCATACGTCTCAACAGGAAAGACGAGGAT	660
Qy	655	CCTAGCGAAGTTTGGGTTATATCGTTTATTCGGTCAAAATGTCGGAGCAACTTCTTAT	714
Db	661	CCTAGCGAAGTTTGGGTTATATCGTTTATTCGGTCAAAATGTCGGAGCAACTTCTTAT	720
Qy	715	GCTGCACTGCGGACGCGGAGGAAACATCTGCGCAATATATACGTTAAATTTTCAC	774
Db	721	GCTGCACTGCGGACGCGGAGGAAACATCTGCGCAATATATACGTTAAATTTTCAC	780
Qy	775	CAAAAACTCTGAATGCGAAGCTGATTAATAAATCAGTATGTCCAAAGAGAGATCTCT	834
Db	781	AGAAAACTTTCAGCGGTCATTAATTAATAAATCAGTATGTCCAAAGAGAGATCTCT	840
Qy	835	AAAAAACCACTGACATTTACGATTTACGATTTACGATTTACGATTTACGATTTACG	894
Db	841	AAAAAACCACTGACATTTACGATTTACGATTTACGATTTACGATTTACGATTTACG	900
Qy	895	AGTGCCTAAGTTAAACACAGAGTGAAGACGATCAGCTGATAAAGATATTTGTTTTC	954
Db	901	AGTGCCTAAGTTAAACACAGAGTGAAGACGATCAGCTGATAAAGATATTTGTTTTC	960
Qy	955	CATACCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTTCGGCATTAAGGGGGAAGCTT	1014
Db	961	CATACCGATGCCGATCAGCGGCTTGAGGGCGGTTTTTTCGGCATTAAGGGGGAAGCTT	1020
Qy	1015	GCCGACGCTTTATCAGAAACGACACAGCGGTTATCGGCTGTTCCGACGCAACAAAA	1074
Db	1021	GCCGACGCTTTATCAGAAACGACACAGCGGTTATCGGCTGTTCCGACGCAACAAAA	1077
Qy	1075	ACAGACGACCAACGATCAGATCAAAATCTCTGCCCTGCGCTCTGGAACACACAAAA	1134
Db	1078	ACAAACGATCAACGACGATCAAAATCTCTGCCCTGCGCTCTGGAACACACAAAA	1137
Qy	1135	ATCTTGGATTTCTTAAAAATTTCCGTTGACGAGCAAGTGGTGAATATCCCGACCGTTT	1194
Db	1138	ATCTTGGATTTCTTAAAAATTTCCGTTGACGAGCGAGTGAATATCCCGACCGTTT	1197
Qy	1195	GAGTTTCCATATGCGGATTTGTTGATCCGACAACTCTTTCGAGGCGCTGAA	1254
Db	1198	GCCATTTTCCCTCTGCGCGGATTTTGGCCATCCCGACAACTCTTTCGAGGCGCTGAA	1257
Qy	1255	ATTCTTTTGTGTAACAAAGAACAAACCATCGATCTTTCGCGGCGGCAAAATGACCGTC	1314
Db	1258	ATTCTTTTGTGTAACAAAGAACAAACCATCGATCTTTCGCGGCGGCAAAATGACCGTC	1317
Qy	1315	CGTCTTGTGTCGATTTTTCACCTATGTGAATCTCGGACGGATTAACCGACGCGCC	1374
Db	1318	CGTCTTGTGTCGATTTTTCACCTATGTGAATCTCGGACGGATTAACCGACGCGCC	1377
Qy	1375	GCCGTCCAAACGAGGCGGATTAAGAGGCGGACGAGGAGGTTAGGCGTTGATAAC	1434
Db	1378	GCAAGTAAACCAAGCGGAGATTAAGAGGCGGATTAAGAGGAGTACAGGCTTGGTAA	1437
Qy	1435	GCTAAGAAAGCGAAGCAAAATCGCGATGAAAGAAACGACCGGAGACGAGTCTGTAGAA	1494
Db	1438	GACGAGAGGACCGGAGATGAAGCGCAGAGGCGAGGAGGCGGAGGCGGAGGAAATC	1497
Qy	1495	GATGAAGACGAGATGAAGACGAGAGAAATCGAAGAA-----GACCTGAA	1542
Db	1498	GCGCATGAAGAGGAGGTGCGGAAGACGAAGCGCGAGAAACCGAAGCGCGAAGAGAC	1557
Qy	1543	GAAGAGCTGAAGAGGAGAAACCGGAAGAGATTCGCGCAGAGAGGCAACGCGGCT	1602
Db	1558	GAAGCTGAAGAACTCGAAGAAACCGGAAGAGATTCGCGCAGAGAGGCGCGGCTGCTGT	1617
Qy	1603	TCAGGACGATCTGCGCCACTTCGGAAGCTCTAAAGCGAGGACATCGACCTTTCTGT	1662
Db	1618	TCAGGACGATCTGCGCCACTTCGGAAGCTCTTAAGCGAGGATATCGACCTTTCTGT	1677
Qy	1663	AAAGGTATCCGCAACGCGGAGCGACATTCGCAAAACCGGAAACCGGCGCATATACCGGC	1722
Db	1678	AAAGGTATCCGCAACGCGGAGCGACATTCGCAAAACCGGAAACCGGCGCATATACCGGC	1737
Qy	1723	ACTTGGGAAGCGGCTATCGGATAGTGTAGTCTCAATTCGCAAAAGGATAGCTAT	1782
Db	1738	ACTTGGGAAGCGGCTATCAGC-----AAACCATTCATGGGACATCAT	1782
Qy	1783	GCG---AATCAAGGGGCAAAAGCAGAAATTTACCGTTGATTTGAAAGCGAAGCGGTGCC	1839
Db	1783	GCGGATAAAAGCGGCAAAAGCAGAAATTTGACGTTGATTTGCGGCGAGAAATCGATTTCC	1842
Qy	1840	GGAATGCTGACAGAAAAAATGATACAAACCCCGCTTTTATATTTGAAAAAGGTGATTT	1899
Db	1843	GGAACGCTGACGGAAGAAAAACGCTGTACAAACCGCTTTTCCATATTTGAAAAACCGGTGAT	1902
Qy	1900	GACGTAACGCTTTCCAGCTTTGCGGATATCTCGGAGAGAGCGGTATTTGACCTTTCTGG	1959
Db	1903	GAGGCAATGCTTTCCAGCTTTGCGGATATCTCGGAGAGAGCGGTATTTGACCTTTCTGG	1962
Qy	1960	CAGGCTGCTGACTAACCCCGAAGAACTTCGAAAGCGGCAATCTTTGTAACAGGCGCTTT	2019
Db	1963	ATGATTCGACTTAATCTTCAAGTTTCAAGCCAAATATCTTTCTGTAACAGGCGCTTT	2022
Qy	2020	TATGCGCCGACGCGGAGAAATTTGGCGGTATATTTATCGACAGCGACCGGAAATTCGTT	2079
Db	2023	TACGCGCCGACGCGGAGAAATTTGGCGGTACTATTTTCAATATGATGGGAAATCTCTT	2082
Qy	2080	GCGGTATTTGGGCGGAAAAAAGATGCAAGGAGGC	2114
Db	2083	GGTATACTGAAGATGCAAAATGAAGCTGAAGC	2117
RESULT 5			
US-10-735-098-1			
; Sequence 1, Application US/10735098			
; Publication No. US20040131634A1			
; GENERAL INFORMATION:			
; APPLICANT: Pettersson-Fernholm, Annika Margareta			
; APPLICANT: Tomassen, Johannes Petrus Maria			
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein			
; FILE REFERENCE: B45106C1			
; CURRENT APPLICATION NUMBER: US/10735,098			
; CURRENT FILING DATE: 2003-12-12			
; PRIOR APPLICATION NUMBER: 09/485,760			
; PRIOR FILING DATE: 2000-02-15			
; PRIOR APPLICATION NUMBER: PCT/EP98/05117			
; PRIOR FILING DATE: 1998-08-10			
; PRIOR APPLICATION NUMBER: GB 9717423.9			
; PRIOR FILING DATE: 1997-08-15			
; PRIOR APPLICATION NUMBER: GB 9805544.8			
; PRIOR FILING DATE: 1998-02-05			
; NUMBER OF SEQ ID NOS: 12			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 1			
; LENGTH: 2277			
; TYPE: DNA			
; ORGANISM: Neisseria meningitidis strain BNCV			
; FEATURE:			
; NAME/KEY: CDS			

i LOCATION: (100)...(2274)
us-10-735-098-1

Query Match		61.0%	Score 1296.2;	DB 17;	Length 2277;
Best Local Similarity		79.0%	Pred. No. 0;		
Matches 1672; Conservative		0;	Mismatches 373;	Indels 72;	Gaps 8;
QY	1	ATGTGTAACCGAATTAAGCGGCAATGTCTGTGTGTCCTTACCTTTTGGCATCTTGATC	60		
Db	100	ATGTGTAACCGAATTAAGCGGCAATGTCTGTGTGTCCTTACCTTTTGGCATCTTGATC	159		
QY	61	GGCGCAATTCGCGGTGCGAGCTGTGTGGAATCAACGCGACCGGTACCCCGTCACT	120		
Db	160	GGCGCAATTCGCGGTGCGAGCTGTGTGGAATCAACGCGACCGGTACCCCGTCACT	219		
QY	121	TTCAAGTCTAAGACGTTTCCACCTTCCTCTCTCCGCGTCTTCGGTAGAAACACACCG	180		
Db	220	TTCAAGTCTAAGACGTTTCCACCTTCCTCTCTCCGCGTCTTCGGTAGAAACACACCG	279		
QY	181	GTCAACCGACCCGCGTGTGTGGGCAATCGCGTGTGTGAGACGGAATATTGCAACTTCT	240		
Db	280	GTCAACCGGCGCGTGTGTGGGCAATCGCGTGTGTGAGACGGAATATTGCAACTTCT	339		
QY	241	GATAAGATGCGAATGATTTTCCAAATAGCAAAACAGCAGAGAAAGCTGTCTGTATAA	300		
Db	340	CGTGAAGATGGCAGGAAATTTCCAAATAGCAAAACAGCAGAGAAAGCTGTCTGTATAA	399		
QY	301	GAGGAAGATATCTGTGTGTATACGCTTCCAAAGAGATCAAGCTGAGAGCTTTAAGAT	360		
Db	400	GAGGTGATGTCTGTGTGTATACGCTTCCAAAGAGATCAAGCTGAGAGCTTTAAGAT	459		
QY	361	AAAAATTCGTAACCAATCTTAGCGCAAGCATTTACACATCGAAGGAAATAAATCAAC	420		
Db	460	GAAATTCATAACGTTGATTCGATGTAGAAATTTAGACATCAGAAAGGAAATAAATAA	519		
QY	421	TATGATTTAAATTTGTAGATGAGTTTATGATATATCTAAAGACGGAAGATGAATTT	480		
Db	520	TATGATTTAAATTTGTAGATGAGTTTATGATATATCTAAAGACGGAAGATGAATTT	576		
QY	481	GAGTGGACTTCAAAATACAGCAGTCTACCAACCGGTTTGGTTATGACGGTTTGTATAT	540		
Db	577	AAGTGGACTTCAAAATACAGCAGTCTACCAACCGGTTTGGTTATGACGGTTTGTATAT	636		
QY	541	TATTCGGAGAACATCTCTTCGCAATCTTTACGAGCGCGGACCGTGAATATTCGCGC	600		
Db	637	TATTCGGAGAACATCTCTTCGCAATCTTTACGAGCGCGGACCGTGAATATTCGCGC	696		
QY	601	AACGTGCAATATACACGATGCGATACGTATCGAACAGGAAAGCAGGAGATCTTAGC	660		
Db	697	AACGTGCAATATATACACGATGCGATACGTATCGAACAGGAAAGCAGGAGATCTTAGC	753		
QY	661	GAGATTTGGGTTATATCGTTTATACGTCGCAATATACGGTTAATTTTCGACCAAAA	720		
Db	754	GACAAATTTGGGTTATATCGTTTATACGTCGCAATATACGGTTAATTTTCGACCAAAA	813		
QY	721	ACTGCCGACGACGGGAGGAAACATCTCCGCAATATACGGTTAATTTTCGACCAAAA	780		
Db	814	AAGGATTCGACGAAAGGAAACATCTCTGCTAAATATACGGTAGATTTTCGGTAAACAA	873		
QY	781	ACTCTGAATGCGAGCTGATTAATAATCAGTATGTGCAAAAGAGAGATGATCTCTAAAAA	840		
Db	874	ACCTTGACGGGAGCTGATTAATAATCAGTATGTGCAAAAGAGAGATGATCTCTAAAAA	930		
QY	841	CCACTGACCAATTTACGACATTTACTGCAAAATTCGACGGCAACCGCTTTACCGGAGTCC	900		
Db	931	CCGCTGACCAATTTACACATCTACTGCGGATTTAAACGCGCAACCGCTTTACCGGAGTCC	990		
QY	901	AAAGTTAACAACAGAGGTGAAGACGATTCAGCTGATAAAGAAATATTGTTTTCATACC	960		
Db	991	AAGGTCAATCTGATTTAGGAAAGCCATGCCAATTAAGAGCATTTGTTTTCATGCC	1050		
QY	961	GATCCGATCAGCGCTTGAGGCGGTTTTTTCGGGATTAAGGGGAAAGCTTTCGCGA	1020		

Db	1051	GATGCCGATCAGCGCTTGAGGCGGTTTTTTTCGCGGATAAGGGGAAGAGCTTCCCGGA	1110
QY	1021	CGGTTTTATCAGCAACGACACAGCGTATTCGGCTGTTTCGAGGCAAAACAAACACAG	1080
Db	1111	CGGTTTTATCAGCAACGACACAGCGTATTCGGCTGTTTCGAGGCAAAACAAACAGCC--	1168
QY	1081	ACAGCAACGCAATCAGATACAAATCCCTGCCCTCGCTCGGAAACACACCAAAATCTTG	1140
Db	1169	-----CCGTGCCGCTCGGAAACACACCAAAATCTTG	1200
QY	1141	GATTCTCTAAATAATTCCTGTGACGAGCAAGTGGTGAATAATCCCGACCGTTTGAGGTT	1200
Db	1201	GATTCTCTGAAATAATTCCTGTGATGAGCAAGTGGTGAATAATCCCGACCGTTTGCAATT	1260
QY	1201	TCCACTATGCCCGATTTTGGTCAATCCCGCAAACTTCTTGTGCAAGGGGTGAATTCCT	1260
Db	1261	TCCTCTATGCCCGATTTTGGTCAATCCCGCAAACTTCTTGTGCAAGGGGTGAATTCCT	1320
QY	1261	TTGGTAAACAAAGAACAAACCATTCGATCTTTCGCGAGCGAGGAAATGACCGTCCGTGCT	1320
Db	1321	TTGGTAAACAAAGAACAAACCATTCGATCTTTCGCGAGCGAGGAAATGACCGTCCGTGCT	1380
QY	1321	TGTTGCGACTTTTGTACCTATGTGAACTCTCGGACGGATAAACCGACCGCCCGCGC	1380
Db	1381	TGTTGCGACTTTTGTACCTATGTGAACTCTCGGACGGATAAACCGACCGCCCGCGC	1440
QY	1381	CAACCGAGCGCGCAGGATGAAGGGGAGCAAGGGGTGTAGGGCTTGATACGGTAAA	1440
Db	1441	AAACCGAGCGCGC-----GGACGAGAGGATTCGACATTCGATATGCGAA	1488
QY	1441	GAAAGCAGAGCAAAATCGCGATGAAGAAACACCGGAGACGAGTCTGAGAGTAA	1500
Db	1489	GAAAGCAGAGCAAAATCGCGATGAAGAAACACCGGAGACGAGTCTGAGAGTAA	1548
QY	1501	GACGAGATGAAGCAAGAAATCGAAGAGAAACCTGAAAGAGAAAGCTGAAGAGGAA	1560
Db	1549	GAAAGCAGAGCAAGAAACGAGCCACAGAAACGAGAGCGGAGAGAGCAAGCTGAA	1608
QY	1561	GAAACCGAGAGAGATTCGCGGCAAGAGCAAGCAACCGCGTTCAGGAGCATCTTCGCC	1620
Db	1609	GAACTGAGAGAGATTCGCGGCAAGAGCAAGCAACCGCGTTCAGGAGCATCTTCGCC	1665
QY	1621	ACTCGGAGAGCTCTAAAGGAGGAGCATCGACCTTTTCTGAAAGTATCGGACGGG	1680
Db	1666	GTCCGGAAGCTCTAAAGGAGGAGCATCGACCTTTTCTGAAAGTATCGGACGGCA	1725
QY	1681	GAAACCGAGATTCGCAAAACCGGACGCAATATACCGGCACTTGGGAGCGGTATC	1740
Db	1726	GAAACGAAATTCGCAAAACCGGACGCAATATACCGGCACTTGGGAGCGGTATC	1785
QY	1741	GGCGTATCGGATAGTGTGCTCCATTCGAAAGAGTATGCTGCGGCACTTGGGAGCGGTATC	1797
Db	1786	GGC-----AAACCAATTCGAAAGAGTATGCTGCGGCACTTGGGAGCGGTATC	1830
QY	1798	AAAGCAGATTTACCGTTGATTTTCGAGCGAGAGCGGTTCGGAATGCTGACAGAAAA	1857
Db	1831	AAAGCAGATTTACCGTTGATTTTCGAGCGAGAGCGGTTCGGAATGCTGACAGAAAA	1890
QY	1858	AATGATACAAACCGCTTTTATATGTAAGAAAGTGTGATTCGCGTAAACGGTTTCCAC	1917
Db	1891	AACGGTGTAGAACCTGTTTCCGTAATGAAACCGGCTGATTCGAGGCAACGGTTTCCAT	1950
QY	1918	GCCTTCGCGCATCTCGGAGAGCGTATGACCTTTCTGGGAGGGTTTGCATAACCCG	1977
Db	1951	GCAGAGCGCGCATCTCGGAGAGCGTATGACCTTTCTGGGAGGGTTTGCATAACCCG	2010
QY	1978	AAGAACTTCAAGCCGACAAATCTTCTGTAAACAGGCGCTTTTATGCGCGGAGCGGCA	2037
Db	2011	CAGATCTTCAAGCTAAATGATCTTCTGTAGAGGAGGATTTTACGCGCGGAGCGGAG	2070
QY	2038	GAAATGGGCGGTAAATATTCGACAGCGACCGAAATTCGGTGGTATTTGGGGGAA	2097
Db	2071	GAAATGGGCGGTAAATATTCGACAGCGACCGAAATTCGGTGGTATTTGGGGGAA	2130

Thu Aug 26 10:18:20 2004

QY 2098 AAAGATGACAAAGGAGGC 2114
Db 2131 GAAATAAAGTTGAAGC 2147

RESULT 6
US-10-735-098-7
; Sequence 7, Application US/10735098
; Publication No. US20040131634A1
; GENERAL INFORMATION:
; APPLICANT: Pettersson-Fernholm, Annika Margareta
; APPLICANT: Tomassen, Johannes Petrus Maria
; TITLE OF INVENTION: Neisseria Lactoferrin Binding Protein
; FILE REFERENCE: B45106C1
; CURRENT APPLICATION NUMBER: US/10/735, 098
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: 09/485, 760
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: PCT/EP98/05117
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: GB 9717423.9
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: GB 9805544.8
; PRIOR FILING DATE: 1998-02-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2262
; TYPE: DNA
; ORGANISM: Neisseria meningitidis strain M990
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2259)
US-10-735-098-7

Query Match 60.8%; Score 1291.8; DB 17; Length 2262;
Best Local Similarity 78.1%; Pred. No. 0;
Matches 1676; Conservative 0; Mismatches 417; Indels 54; Gaps 8;
QY 1 ATGTGTAAACCGAATTATGCGGCATGCTCTGTGGCCCTTACTTTTGGCATCTTGATC 60
Db 1 ATGTGTAAACCGAATTATGCGGCATGCTCTGTGGCCCTTACTTTTGGCATCTTGATC 60
QY 61 GCGCGCAATTTCGCGGTGACGCTGTGTGCAATCAACGCGGACCGG----- 108
Db 61 GCGCGCAATTTCGCGGTGACGCTGTGTGCAATCAACGCGGACCGGCGCAACTCTGTCA 120
QY 109 TACCCGCTCACTTCAAGTCAAGGACGTTCCCACTTCGCTCTCGCGGTCTTCGGTA 168
Db 121 GATTCCAAATCTTCCAAATCTCGCGGATAAGCTCTGCTCAGCTCTCGCGGACCTTCGGTA 180
QY 169 GAAACACGCGGTCAACGACCGCGGTGTGGTGGGCAATGCGGCTGTGTGAGACGGAAT 228
Db 181 GAAATACGCGGTCAACGACCGCGGTGTGGTGGGCAATGCGGCTGTGTGAGACGGAAT 240
QY 229 ATTGCAACTTCTGATAGGATGCGCAATGATTTTCAATAGCAACAGAGAGAGAAAG 288
Db 241 ATCGCACTTTGATAAAAATGGTAATGAAATTCCAATAGTAAGCAGGAGAGATAT 300
QY 289 CTGTCGTTTAAAGAGGAGATATCTGTGTTTATACGGTTCCTGTTTAAAGAGATCAAGCTCAG 348
Db 301 CTGCGGCTCAAGAGAGGATATCTGTGTTTATAGCGGTACGCCGAAAGACAGGCTGAC 360
QY 349 CAGCTTAAGATATAATTCGTCAACCAATCTTACGCGAAGCATTTACCAATTCGGAAG 408
Db 361 AAATTTAAAGGAATCAACGCGGCTCTTAATGACCAATCTACAGCTCCGATTTA 420
QY 409 AAAAAATAAAAAATATGATATAAATTTGTAGATGAGGTTATGATATATCTAAAGACGGA 468
Db 421 AAAGATGATGCTATCAATATAAATATGTCCGGCGGATATGTTTATACATGATGGA 480
QY 469 AAAGATGAAATTTAGTGGAGTCTCAATATACAGGAGTCTTACCAACCGGTTTGGTTATGAC 528

Db 481 ACAGATGAAATCGAACAGAACTCAGGCGGTAAAGCGGTATCCACCGCTTAGGTTATGAC 540
QY 529 GGTGTTGATATATTCGCGAGAACATCTTTCGCAATCTTTTACCGAGCGGGAACGGTG 588
Db 541 GGTGTTGATATATTCGCGAGAACGCTCTTCCCAATCTTTTACCGAGTGGGGAACGGTG 600
QY 589 AAATATTCCGCAACTGCGCAATATGACCGATGCCATACGCTATCGAACAGGAAGCA 648
Db 601 GAATATTCTGTAATCTGCAATATGACCGATGCCAATCTATCGAGAGGTCAGGC- 659
QY 649 GGAGATCTAGCGAAGATTTGGGTATATCTGTTTATACGCTCAAAATGTCGAGCAACT 708
Db 660 --GGTTGGCAATTGCAATTTGGGTATATCACTTTATGTTAAGATGTTGTTGCACT 717
QY 709 TCTTATGCTGCGACTGCGCAGCAGCGGAGGAGAAACATCTCTGCCAATATACGTTAAT 768
Db 718 TCTTATGCGCTAAGGATGTGACGAAAGGAAAGCATCTCTGCCAATATACGTTGAT 777
QY 769 TTGACCAAAAAAATCTGAAATGGCAAGCTGATTAATAATCAGTATGTC--AAAGAGA 825
Db 778 TTTGATAACAAAAATCATGATGGCAAGCTGATTAATAATCAGTATGTCGAAATATAA 837
QY 826 GATGATCTTAAATAACCACTGACCATTTACGACATTTACTGCAAAATGACGCGCAAC 885
Db 838 GATGAACCCAAAAACCGCTGACCATTTACGACATTTACTGCAAAATGACGCGCAAC 897
QY 886 TTTTACCGCAGTGCCAAAGTTAAACACAGAGGTGAAGACGAATCACGCTGATTAAGA 945
Db 898 TTTTACCGCAGTGCCAAAGTTAAACAGTCAATCTGATTTAGCGAAAACTTCCGCT 957
QY 946 TTGTTTTCCTACCGATGCCGATCAGCGCTTGGAGGCGGTTTTTCCGCGATAGGGG 1005
Db 958 TTGTTTTCCTACCGATGCCGATCAGCGCTTGGAGGCGGTTTTTCCGCGATAGGGG 1017
QY 1006 GAAGAGCTTCCGCGAGCGTTTATCAGCAACGACCAACAGCGTATTCGCGCTGTTCG 1065
Db 1018 GAAGAGCTTCCGCGAGCGTTTATCAGCAACGACCAACAGCGTATTCGCGCTGTTCG 1077
QY 1066 AAACAAAAACAGACAGCAGCAACCGCATCAGATACAAATCTCTGCCCTGCGCTCTG 1125
Db 1078 A---AAACAAACAGACAGCAGCAACCGCATCAGATACAAATCTCTGCCCTGCG 1134
QY 1126 CACACCAAAATCTTGAATCTCTAAATAATTCGTTGACGACCAAGTGTGAAATATCC 1185
Db 1135 CACACCAAAATCTTGAATCTCTAAATAATTCGTTGACGAGGCGATGATGCGCATGCC 1194
QY 1186 CGACCGTTGAGGTTTCCACTATGCGCGATTTTGGTCTATCCGACAAACTTTTGTG 1245
Db 1195 CGTAAGTTTCCGCTTCTCTATGCCGATTTTGGTCTATCCGACAAACTTTTGTG 1254
QY 1246 GGGCGTGAATTTCTTTGTTAAACAAAGACAAACCAATCGATCTTGGCGAGCGGAG 1305
Db 1255 GGGCGTGAATTTCTTTGTTAAACAAAGACAAACCAATCATCAAGCTTGGCGAG 1314
QY 1306 ATGACCGTCCGTTGTTGCGATTTTGGACCTATGTAACCTCGGACGATATAAAC 1365
Db 1315 ATGACCGTCCGTTGTTGCGATTTTGGACCTATGTAACCTCGGACGATATAAAC 1374
QY 1366 GAACGCGCGCGTCCAAACGAGCGCAGGATCAAGAGGGGAGGAGAGAGGGTGTAG 1425
Db 1375 GATCGCGCGGCAAGTAACCAAGCGGAGATTAAGGGAGGATGAAGAGGTCAGGC 1434
QY 1426 GTTGATAACGGTAAAGAAAGCAAGAGCAATCGCGCATGTAAGAAAGCACCGGAG 1485
Db 1435 GTTGATAACGACGAGAAAGCAAGAGCAAGCGCTAGAAAGACGAGCGGCGGAG 1494
QY 1486 G-----TCGTAGAGATGAAGACGAAATCAAG------CGAAGAGAAATCG 1530
Db 1495 GAACTTCCGAAGAGGATTAATGGCGAAGACGAGAGAGCAACCGCGAGAGAAC 1554
QY 1531 GAAGAGCTGAGAGAGAGCTCAAGAGGAGAAACCGGAGAGAAATTCGCGCAGAG 1590

QY 1454 AAATCGGCGATGAGAAAGCACCGGAGACGAAGTCGTAGAAATGATGAACGGAATGAAG 1513

; PRIOR APPLICATION NUMBER: US

PRIOR APPLICATION N

PRIOR APPLICATION NUMBER: US 09/747,377

1165	GAGCGAAGTGGTCAAAATCCCGACCGTTTGAGGTTCCACATGCCCCGATTTGGTGCAT	1224
9462	GAGCGANNN	9403
1225	CCCGCAAACTTCTGTGCAAGGCGTGAAATTCCTTTGTATAACAAGAACAAACCATC	1284
9402	NN	9343
1285	GATCTTCCGACGGCAGGAAATGACCGTCGGTGTGGCACTTTTGCACCTATGTG	1344

[illegible]

Qy 1569 AGAAGAATTGCCGCGAGAAGAGGCAAG 1597
| | | | |
Db 43 AGAAGAAGAAGAAGAAAAATTTAAG 15

Search completed: August 25, 2004, 14:58:25
Job time : 1076.14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 11:49:00 ; Search time 4846.67 Seconds
(without alignments)
13086.780 Million cell updates/sec

Title: US-10-735-098-9
Perfect score: 2124
Sequence: 1 atgtgtaaaccgaattatgg.....acaaggaggcaacacgatga 2124

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_est3:*
13:	gb_est4:*
14:	gb_est5:*
15:	em_estfun:*
16:	em_estom:*
17:	em_gss_hum:*
18:	em_gss_inv:*
19:	em_gss_pln:*
20:	em_gss_vrt:*
21:	em_gss_fun:*
22:	em_gss_mam:*
23:	em_gss_mus:*
24:	em_gss_pro:*
25:	em_gss_rod:*
26:	em_gss_phg:*
27:	em_gss_vrl:*
28:	gb_gss1:*
29:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	103.4	4.9	531	14	CD915362
2	101	4.8	802	28	BH066160
C 3	100.8	4.7	434	14	CA745444
C 4	99.4	4.7	289	14	CA716220

5	99.2	4.7	223	13	CA022136
6	99	4.7	395	29	CE760553
7	98.8	4.7	264	13	BQ241566
8	98.6	4.6	729	29	CE180020
C 9	98.6	4.6	1096	14	CK206118
10	97.6	4.6	799	28	BZ201507
11	97.4	4.6	575	10	BF707975
C 12	97.2	4.6	232	29	CG321416
C 13	97.2	4.6	233	12	BJ745017
C 14	97.2	4.6	691	28	BH040136
15	97	4.6	675	28	BZ104011
16	96.8	4.6	278	13	BQ460618
17	96.8	4.6	744	28	BH065422
C 18	96.8	4.6	774	28	AZ658872
19	96.6	4.5	477	14	CD111846
20	96.6	4.5	960	28	CC143364
C 21	96.4	4.5	283	13	BU005139
22	96.2	4.5	719	28	BH360392
C 23	95.8	4.5	311	14	CA699402
24	95.8	4.5	980	13	BU944408
25	95.6	4.5	332	14	CA566759
C 26	95.6	4.5	605	28	BZ222147
27	95.6	4.5	617	14	CA743799
28	95.4	4.5	205	13	BQ241058
C 29	95.4	4.5	546	28	AZ600777
30	94.8	4.5	341	29	CE510654
31	94.6	4.5	924	13	BQ925195
32	94.2	4.4	340	13	BQ462203
C 33	94	4.4	483	28	AZ060017
34	94	4.4	527	28	AZ279446
35	94	4.4	596	29	CG660549
C 36	93.8	4.4	613	29	CE357285
C 37	93.8	4.4	880	28	AZ529191
38	93.8	4.4	953	13	BQ939407
39	93.6	4.4	293	13	BQ459561
40	93.6	4.4	295	13	BU976670
41	93.6	4.4	665	13	BU432980
42	93	4.4	342	11	AY383662
43	93	4.4	537	14	CF380795
44	92.8	4.4	358	28	AZ582992
45	92.8	4.4	495	14	CD663452

ALIGNMENTS

RESULT 1
CD915362

LOCUS
DEFINITION

CD915362
G550.125001F010713 G550 Triticum aestivum cDNA clone G550125001,
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

531 bp mRNA linear EST 14-JUL-2003
Triticum aestivum (bread wheat)
GI:32689686
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 531)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)
and <http://genoplante-info.infobiogen.fr>.

FEATURES

source

1. .531

QY 1382 AACGAAGCGGACGATGAAGAGGGGACGAAGAGGTTGTAGCGTTGATACCGTAAAG 1441
 Db 381 AAGTGGAGAGGAG 322
 QY 1442 AAGCGAAGACGAATCGCGGATGAAGAAAGCACCGGAGACGAAGTCTGTAGAGATGAAG 1501
 Db 321 AAGAAG 262
 QY 1502 ACGAAGATGAAGACGAAG 1561
 Db 261 AAGAAG 202
 QY 1562 AACCGAAGAGAGATTCGCGGCGAGAGAGAG 1591
 Db 201 AAGAAG 172

RESULT 4
 CA716220/c
 LOCUS
 DEFINITION
 289 bp mRNA linear EST 26-NOV-2002
 wdk3c.pk024.i22 wdk3c Triticum aestivum cDNA clone wdk3c.pk024.i22
 5' end, mRNA sequence.

ACCESSION
 VERSION
 SOURCE
 CA716220
 CA716220.1 GI:25438013
 EST.
 Triticum aestivum (bread wheat)
 ORGANISM
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,
 Miao, G., Caraher, N. and Hanafey, M.K.
 DuPont Wheat cDNA Sequence
 Unpublished (2002)
 Contact: Scott V. Tingey
 Crop Genetics
 E. I. DuPont de Nemours and Company
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
 Tel: 302-631-2602
 Fax: 302-631-2607
 Email: Scott.V.Tingey@USA.dupont.com
 Seq primer: M13.

FEATURES
 source
 Location/Qualifiers
 1..289
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone="wdk3c.pk024.i22"
 /tissue_type="kernel"
 /lab_host="DH10B"
 /clone_lib="wdk3c"
 /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
 XhoI; Wheat (Triticum aestivum L.) developing kernel, 14
 days after anthesis."

ORIGIN
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 Best Local Similarity 67.5%; Pred. No. 1.7e-09;
 Matches 139; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
 QY 1386 GAAGCGGAGGATGAAGAGGGGACGAAGAGGTTGTAGCGTTGATACCGTAAAGAG 1445
 Db 252 GAAGATGACGAGGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 193
 QY 1446 CGAAGACGAATTCGCGGATGAAGAAAGCACCGGAGACGAAGTCTGTAGAGATGAAGAG 1505
 Db 192 AAGAAG 133
 QY 1506 AGATGAAGACGAAGAGAAATTCGAAGAGAACTCGAAGAGAAAGCTGAAGAGGAGAAC 1565
 Db 132 AAGAAG 73

QY 1566 CGAAGAGAAATTCGCGGACGAAGAGAG 1591
 Db 72 AAGAAG 47

RESULT 5
 CA022136
 LOCUS
 DEFINITION
 223 bp mRNA linear EST 23-OCT-2002
 H242R07r HZ Hordeum vulgare subsp. vulgare cDNA clone H242R07
 5-PRIME, mRNA sequence.

ACCESSION
 VERSION
 SOURCE
 CA022136
 CA022136.1 GI:24299510
 EST.
 Hordeum vulgare subsp. vulgare
 ORGANISM
 Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.
 Barley ESTs from developing seeds
 Unpublished (2002)
 Contact: Stein Nils

Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de

Insert length: 223 Std Error: 0.00
 Plate: 42 row: E column: 7
 Seq primer: M13rev.

FEATURES
 source
 Location/Qualifiers
 1..223
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 /mol_type="mRNA"
 /cultivar="barke"
 /sub_species="vulgare"
 /db_xref="GABI:275541"
 /db_xref="taxon:112509"
 /clone="HZ42E07"
 /tissue_type="pericarp"
 /dev_stage="0-7 DAP (days after pollination)"
 /lab_host="XL10-Gold"
 /clone_lib="HZ"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
 cDNA); Site 2: XhoI (3'-end of cDNA); pericarp 0-7
 DAP(days after pollination). Due to a cloning artefact
 caused by the kit, in most cases the EcoRI site is NOT
 present, as well as the EcoRI adapter used for cloning. To
 excise the insert, restriction sites upstream EcoRI should
 be used (e.g. BamHI, Sall, EstI). NOTE: Also due to the
 cloning system used Blue/white selection for recombinants
 is not 100% reliable. Average insert size is 900 bp"

ORIGIN
 Query Match 4.7%; Score 99.2; DB 13; Length 223;
 Best Local Similarity 67.3%; Pred. No. 1.8e-09;
 Matches 140; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
 QY 1384 CCGAAGCGGAGGATGAAGAGGGGACGAAGAGGTTGTAGCGTTGATACCGTAAAGAA 1443
 Db 1 CGGCACGAGGAG 60
 QY 1444 AGCGAAGACGAATTCGCGGATGAAGAAAGCACCGGAGACGAAGTCTGTAGAGATGAAGAC 1503
 Db 61 GAAGAAGAGGAG 120
 QY 1504 GAAGATGAAGACCAAGAGAGAAATTCGAAGAGAACTCGAAGAGAAAGCTGAAGAGGAGAGAA 1563
 Db 121 GAAGAAG 180

[illegible]

REFERENCE

1 (bases 1 to 729)
 Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 22875432
 14512627
 PUBMED
 COMMENT
 Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES

Location/Qualifiers
 1..729
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /notes="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 4.6%; Score 98.6; DB 29; Length 729;
 Best Local Similarity 67.8%; Pred. No. 2.5e-09;
 Matches 140; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
 QY 1386 GAAGCGCAGGATGAGAGCGGACGAGAGGCGTAGCGTTGATACGTTAAGAAAG 1445
 DB 168 GAAGAAG 227
 QY 1446 CGAAGACGAATCGGCGATGAAGAAGACCGGAGACGAGTGTGTAAGAGATGAAGACCA 1505
 DB 228 AGAAGAAG 287
 QY 1506 AGATCAAGACGAG 1565
 DB 288 AGAAGAAG 347
 QY 1566 CGAAGAAGATTCGCGCAGAGAGAGGCA 1594
 DB 348 AGAAGAAGATTAGGATCAATATATGCA 376

RESULT 9

CK206118/c
 LOCUS
 DEFINITION FGAS017695 Triticum aestivum FGAS: Library 5 GATE 7 Triticum
 aestivum cDNA, mRNA sequence.
 CK206118
 VERSION
 CK206118.1 GI:39568508
 EST.
 Triticum aestivum (bread wheat)
 ORGANISM

REFERENCE

1 (bases 1 to 1096)
 Allard, R., Crosby, W.L., Danyluk, J., Eudes, P., Frick, M., Gaudet, D.,
 Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
 Links, M.G., McFarthy, E.L., Monroy, A., Muzak, I., Nilson, D.,
 Penniket, C., Roach, J.L. and Sarhan, F.
 Functional Genomics of Abiotic Stress In Wheat and Canola Crops
 Unpublished (2003)
 Contact: Wm L Crosby
 Bioinformatics
 University of Saskatchewan, Department of Computer Science
 1C101 Engineering Building, 57 Campus Drive, Saskatoon,
 Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769
 Fax: 306 966 2033
 Email: fgas_est@cs.usask.ca

This sequence is the direct result of the Base calling software
 Phred (default parameters). It is the raw base calls. To aid in the
 identification of the high quality insert the software Lucy
 (default parameters) has been run on this sequence. Lucy identified
 the region [29,696].

Plate: LSB006 row: F column: 12.

FEATURES

Location/Qualifiers
 1..1096
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone_lib="Triticum aestivum FGAS: Library 5 GATE 7"
 /notes="Vector: PCMV.SPORT6; Crown and developmental stages
 of spike formation in wheat cultivar Norstar. 4 mRNA
 populations were combined before constructing the library.
 The first mRNA population is from 1cm crown sections after
 30 days of cold acclimation. The second is from 1cm crown
 sections after 11 days of deacclimation (before
 deacclimation plants were fully vernalized for 49 days).
 The third is from different developmental stages of spike
 formation (5 to 50mm) that still have not emerged from the
 leaf (dissection required). The last is from different
 developmental stages of spike and seed formation after
 having emerged from the leaf (visible). First strand
 synthesis in this library was done in the presence of
 methylated dCTP thereby protecting from internal cleavage
 with NotI."

ORIGIN

Query Match 4.6%; Score 98.6; DB 14; Length 1096;
 Best Local Similarity 63.9%; Pred. No. 2.6e-09;
 Matches 149; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
 QY 1359 AAAAACCGAACCCCGCGTCCAAACCGAAGCGCAGGATGAAGAGGGGAGAGAGGG 1418
 DB 300 AGAACCAAGAGACCCCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 241
 QY 1419 TGTAGCGTTGTATACGTTAAGAAAGCGAAGACGAAATCGCGCATGAAGAAAGCACC 1478
 DB 240 AGAAGAAG 181
 QY 1479 AGACGAAGTCTGTAGAGATGAAGCAGATGAAGCAGAGAAATCGAAGAGAAACC 1538
 DB 180 AGAAGAAG 121
 QY 1539 TGAAGAAGAGCTGAAGAGAGAGAACCCGAGAGAGAAATTCGCGCAGAGAGAG 1591
 DB 120 AGGAGAAG 68

RESULT 10

BZ201507
 LOCUS
 DEFINITION BZ230-445016 TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
 CH230-445016, genomic survey sequence.
 BZ201507
 ACCESSION
 BZ201507.1 GI:23859559
 VERSION
 BZ201507.1
 KEYWORDS
 GSS.
 SOURCE
 Rattus norvegicus (Norway rat)
 ORGANISM
 Rattus norvegicus
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 799)
 REFERENCE
 1 (bases 1 to 799)
 AUTHORS
 Zhao, S., Shetty, J., Shatsman, S., Tsagaye, G., Geer, K.,
 Shvartsbeyn, A., Gebregorgis, E., Overton, L., Russell, D., Chen, D.,
 Riggs, F., de Jong, P. and Fraser, C.M.
 Rat BAC End Sequences from Library CHORI-230 MboI segment
 Unpublished (1999)
 Other_GSSs: CH230-445016.TV


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/clone_lib="ZM_0.7_1.5_KB"  
/note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"
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	Best Local Similarity	4.6%;	Pred. No.	4.5e-09;	
	Matches 135; Conservative	0;	Mismatches	63;	Indels
		0;	Gaps	0;	
QY	1394 AGGATCAAGAGGGGGCGAGAGGGTGTAGCGTTGATACGGTAAAGAAGCGAAGACG	1453			
Dd	214 AAGATGGAAG	155			
QY	1454 AAATCGCGGATGAAGAAAGCACCGGAGACGAACTCTTAGAAGATCAAGACGAAGATCAAG	1513			
Dd	154 AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	95			
QY	1514 ACAGAAGAAGAAATCGAAGAAGAACCTGAAGAGAAAGCTGAAGAGAGAAACC CGAAGAAG	1573			
Dd	94 AAGAAGAAGAAGAAG	35			
QY	1574 AATTCCCGCAGAGAAG	1591			
Dd	34 AAGAAGAAGAAGAAGAAG	17			

RESULT 13	Bu454017/c
LOCUS	Bu454017 K. Sato unpublished cDNA library, cv. Akashinriki
DEFINITION	vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak45jl5 5', mRNA sequence.
ACCESSION	Bu454017
VERSION	Bu454017.1 GI:21132592
KEYWORDS	EST.
SOURCE	Hordeum vulgare subsp. vulgare
ORGANISM	Hordeum vulgare subsp. vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum. 1 (bases 1 to 233)
REFERENCE	Sato, K., Saisho, D. and Takeda, K.
AUTHORS	Barley EST sequencing project in NIG and Okayama Univ
TITLE	Unpublished (2002)
JOURNAL	Contact: Tadasu Shin-i
COMMENT	Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp.

```

FEATURES
source
email: tsunagi@genes.nig.ac.jp.
location/Qualifiers
1..233
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/sub_species="vulgare"
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/clone="baak45j15"
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/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA library"
Akashinriki vegetative stage leaves

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[illegible]

Qy	1454	AATTCGCGATGAAGAAACACCCGGAGAGAAGTCTGAGAGATGAAGACGAACATCAAG	1513
Db	141	AGCAAGACCAAGAGAGAGAAANGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	82
Qy	1514	ACGAGAAGAAATCGAAGAAGAACCTGGAAGAAGACTGAAGAGGAGAAACC CGAAGAAG	1573
Db	81	AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAGAGAGAGATGAAGTGAAGAAGAAGAAG	22
Qy	1574	AATTGCCGCAGAGAAG	1591
Db	21	AACAAGAACTAGAAGAAG	4

RESULT 14
 BH040136/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Other GSs: RPCI-24-255A23.TU
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choiri.org/bacpac/orderingframe.htm>). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 255 row: A column: 23
Seq primer: T7
Class: BAC ends.

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FEATURES
source
Class: BAC ends.
Location/Qualifiers
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/clone_lib="RPCI-24"
/note="Vector: pTARBAC1;
RPCI-24 Mouse BAC Library
library was cloned in the
BamHI sites using MboI p
DNA."

```

ORIGIN

[illegible]

